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OM protein - protein search, using sw model

Run on: December 18, 2004, 01:06:47 ; Search time 113.524 Seconds
(without alignments)
1425.134 Million cell updates/sec

Title: US-09-676-249D-2

Perfect score: 2299
Sequence: 1 MKKKIKWKKFGLGLVPLP.....KOPDKQESDILITDINKN 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	2299	100.0	451	AAU01859	AAU01859 Mycoplasma
2	2299	100.0	451	AAO15861	AAO15861 Mycoplasma
3	2134	92.8	423	AAO15862	AAO15862 Mutant My
4	2109	91.7	423	AAU01860	AAU01860 Mycoplasma
5	714.5	31.1	453	AAK40856	AAK40856 43kd Tegr
6	706	30.7	457	AAO15867	AAO15867 Mycoplasma
7	694.5	30.2	432	AAK67582	AAK67582 Cancer me
8	655	28.5	448	AAK93343	AAK93343 Gene enco
9	394.5	17.2	428	AAV05332	AAV05332 Inflammat
10	394.5	17.2	428	ABP71709	ABP71709 M161 anti
11	393.5	17.1	428	ADK68531	ADK68531 Mycoplasma
12	390.5	17.0	428	ADK68538	ADK68538 Mycoplasma
13	387.5	16.9	429	AAW22727	AAW22727 Membrane
14	384.5	16.7	404	ADK68536	ADK68536 Mycoplasma
15	381.5	16.6	404	ADK68537	ADK68537 Mycoplasma
16	232.5	10.1	350	ABP25843	ABP25843 Streptococ
17	232.5	10.1	350	ABG66912	ABG66912 Streptococ
18	227	9.9	351	AAV81632	AAV81632 Streptococ
19	225	9.8	363	ADK46171	ADK46171 Streptococ
20	223	9.7	350	ABU01234	ABU01234 S. pneumo
21	217.5	9.5	330	ABG66916	ABG66916 Streptococ
22	217.5	9.5	330	ABG66915	ABG66915 Streptococ
23	215.5	9.4	349	ABP27752	ABP27752 Streptococ
24	214.5	9.3	330	ABG66917	ABG66917 Streptococ
25	207	9.0	350	ABB54779	ABB54779 Lactococc

26	203	8.8	328	2	AAW55066	AAW55066 Streptococ
27	203	8.8	328	5	ABP54560	ABP54560 S. pneumo
28	203	8.8	328	7	ADC45089	ADC45089 S. pneumo
29	203	8.8	374	7	ADC95457	ADC95457 E. faecali
30	199.5	8.7	362	7	ADH88119	ADH88119 Enterococ
31	197	8.6	347	5	ABP30886	ABP30886 Streptococ
32	197	8.6	347	5	ABP29678	ABP29678 Streptococ
33	197	8.6	370	5	ABP25842	ABP25842 Streptococ
34	188.5	8.2	347	5	ABP29943	ABP29943 Streptococ
35	188.5	8.2	347	5	ABG66913	ABG66913 Streptococ
36	188	8.2	366	6	ADB09398	ADB09398 Alloiococ
37	182	7.9	339	2	AAV00049	AAV00049 Enterococ
38	182	7.9	339	5	ABP43268	ABP43268 E. faecali
39	182	7.9	339	6	ABU88296	ABU88296 E. faecali
40	182	7.9	339	6	ABU13547	ABU13547 Enterococ
41	182	7.9	361	2	AAV00048	AAV00048 Enterococ
42	182	7.9	361	5	ABP43267	ABP43267 E. faecali
43	182	7.9	361	6	ABU88295	ABU88295 E. faecali
44	182	7.9	361	6	ABU13546	ABU13546 Enterococ
45	182	7.9	375	7	ADH88120	ADH88120 Enterococ

ALIGNMENTS

RESULT 1	
ID	AAU01859 standard; protein: 451 AA.
XX	AAU01859;
AC	AAU01859;
DT	07-SEP-2001 (first entry)
XX	
DE	Mycoplasma hyopneumoniae MHP3 antigen.
XX	
KW	MHP3; antigen; vaccine; enzootic mycoplasma pneumonia; antibody;
KM	immunoassay; immunotherapy; anti-idiotypic antibody.
XX	
OS	Mycoplasma hyopneumoniae.
XX	
FN	Key
FT	Misc-difference 7 Location/Qualifiers
FT	Misc-difference 7 /note= "Encoded by TGA"
FT	Misc-difference 99 /note= "Encoded by TGA"
FT	Misc-difference 138 /note= "Encoded by TGA"
FT	Misc-difference 152 /note= "Encoded by TGA"
FT	Misc-difference 174 /note= "Encoded by TGA"
FT	Misc-difference 198 /note= "Encoded by TGA"
FT	Misc-difference 246 /note= "Encoded by TGA"
XX	
PN	EP1090995-A2.
PD	11-APR-2001.
XX	
PE	26-SEP-2000; 2000EP-00308421.
XX	
PR	29-SEP-1999; 99US-0156602P.
XX	
PA	(PRIZ) PRIZER PROD INC.
PI	King KW, Madura RA, Rosey EL;
XX	
DR	WPI: 2001-309781/33.
XX	
PT	N-PSDB: AAS03285.
PT	New apoprotein antigens encoded by mhp3 gene from Mycoplasma hyopneumoniae useful as a vaccine for treating or preventing diseases

PT caused by Mycoplasma hyopneumoniae.
 XX
 PS Claim 11; Page 17-18; 38pp; English.
 XX
 CC The sequence is Mycoplasma hyopneumoniae Mhp3 antigen. Mhp3 antigen and
 CC its fragments are useful in manufacturing a vaccine for treating or
 CC preventing a disease or disorder in an animal, especially pig, caused by
 CC M. hyopneumoniae infection e.g. enzootic mycoplasma pneumonia. The mhp3-
 CC encoded proteins may be used as immunogens to generate antibodies which
 CC immunospecifically bind such an immunogen. The antibodies generated
 CC against the antigen are useful in diagnostic immunoassays, passive
 CC immunotherapy and generation of anti-idiotypic antibodies. Mhp3 proteins
 CC may also be used in immunoassays, e.g. to detect or measure in a
 CC biological sample from a vaccinated or potentially infected test animal
 CC the presence of antibodies to the antigen, and thus to monitor the immune
 CC response and/or to diagnose infection of the animal
 CC
 XX
 SQ Sequence 451 AA;

Query Match 100.0%; Score 2299; DB 4; Length 451;
 Best Local Similarity 100.0%; Pred. No. 1,4e-164;
 Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKKIKNNKFLGLVPEPLSAIATISAGCWDKETTKEKSDADNOKQITDVSKISGLVNE 60
 DB 1 MKKKIKNNKFLGLVPEPLSAIATISAGCWDKETTKEKSDADNOKQITDVSKISGLVNE 60
 QY 61 RKSEIMAKADANHFGLNMAIYTAGTVNDNSFNQSSWEAIQOLGALTGEITVSVDST 120
 DB 61 RKSEIMAKADANHFGLNMAIYTAGTVNDNSFNQSSWEAIQOLGALTGEITVSVDST 120
 QY 121 AELEGGTSSLANTNNKNWVLSGFQHGDAFTRWLKIPEKNKIIILIGIDWTDTEENV 180
 DB 121 AELEGGTSSLANTNNKNWVLSGFQHGDAFTRWLKIPEKNKIIILIGIDWTDTEENV 180
 QY 181 IPGRYINLTYKTEBAGWLAGYANASFLAKKPSDPTKRSALVIGGGSIPAVTDFIAGYL 240
 DB 181 IPGRYINLTYKTEBAGWLAGYANASFLAKKPSDPTKRSALVIGGGSIPAVTDFIAGYL 240
 QY 241 AGIKAWNLKNSDKKTKITTDKIEINLGFVDQSTKERLEQIASKDKPSTLLAVAGPLTE 300
 DB 241 AGIKAWNLKNSDKKTKITTDKIEINLGFVDQSTKERLEQIASKDKPSTLLAVAGPLTE 300
 QY 301 IFSDIIANQNDRYLIGVTDQSLVYTKTKNKFPTSIILKNLGYSVFSVLSDLYTKKSNSRN 360
 DB 301 IFSDIIANQNDRYLIGVTDQSLVYTKTKNKFPTSIILKNLGYSVFSVLSDLYTKKSNSRN 360
 QY 361 LAGFEPGKSAATVYLGIDKDFVDIADTSLSEGNKKLATSEAKKEPEEKTKTIPAEV 420
 DB 361 LAGFEPGKSAATVYLGIDKDFVDIADTSLSEGNKKLATSEAKKEPEEKTKTIPAEV 420
 QY 421 RKTLEIPMPDKQPDKOESLDKLITDINKN 451
 DB 421 RKTLEIPMPDKQPDKOESLDKLITDINKN 451

RESULT 2
 AAO15861
 ID AAO15861 standard; protein; 451 AA.
 XX
 AC AAO15861;
 XX
 DT 16-JAN-2003 (first entry)
 XX
 DE Mycoplasma hyopneumoniae mhp3 protein.
 XX
 KW Apoptein antigen; enzootic mycoplasma pneumonia; mhp3; vaccine;
 KM Mycoplasma hyopneumoniae infection.
 XX
 OS Mycoplasma hyopneumoniae.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 7

FT /note= "Encoded by TGA"
 FT Misc-difference 99
 FT /note= "Encoded by TGA"
 FT Misc-difference 138
 FT /note= "Encoded by TGA"
 FT Misc-difference 152
 FT /note= "Encoded by TGA"
 FT Misc-difference 174
 FT /note= "Encoded by TGA"
 FT Misc-difference 198
 FT /note= "Encoded by TGA"
 FT Misc-difference 246
 FT /note= "Encoded by TGA"
 FT
 PN EP1245677-A1.
 PD
 PD 02-OCT-2002.
 PP 30-MAR-2001; 2001EP-00303030.
 PR 30-MAR-2001; 2001EP-00303030.
 PA (Pfizer) Pfizer Prod Inc.
 PI King KM, Madura RA, Rosey EL;
 DR WPI; 2002-742716/81.
 DR N-PSDB; AAL50632.
 XX
 PT Novel apoprotein antigens encoded by Mycoplasma hyopneumoniae for use in
 PT vaccines to prevent and treat diseases caused by infection with
 PT Mycoplasma hyopneumoniae in animals, especially pigs.
 PS
 PS Claim 11; Fig 1; 38pp; English.

XX The invention comprises the amino acid and coding sequences of Mycoplasma
 CC hyopneumoniae mhp3 proteins, the invention also comprises novel
 CC apoprotein antigens encoded by the M. hyopneumoniae mhp3 gene. M.
 CC hyopneumoniae is a bacterial pathogen that causes enzootic mycoplasma
 CC pneumonia in pigs. The mhp3 genes, proteins and apoprotein antigens of
 CC the invention are useful in the manufacture of a vaccine for treating/
 CC preventing a disease or disorder caused by infection with M.
 CC hyopneumoniae in an animal, especially a pig. The present amino acid
 CC sequence represents a Mycoplasma hyopneumoniae mhp3 protein of the
 CC invention

SQ Sequence 451 AA;

Query Match 100.0%; Score 2299; DB 5; Length 451;
 Best Local Similarity 100.0%; Pred. No. 1,4e-164;
 Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKKIKNNKFLGLVPEPLSAIATISAGCWDKETTKEKSDADNOKQITDVSKISGLVNE 60
 DB 1 MKKKIKNNKFLGLVPEPLSAIATISAGCWDKETTKEKSDADNOKQITDVSKISGLVNE 60
 QY 61 RKSEIMAKADANHFGLNMAIYTAGTVNDNSFNQSSWEAIQOLGALTGEITVSVDST 120
 DB 61 RKSEIMAKADANHFGLNMAIYTAGTVNDNSFNQSSWEAIQOLGALTGEITVSVDST 120
 QY 121 AELEGGTSSLANTNNKNWVLSGFQHGDAFTRWLKIPEKNKIIILIGIDWTDTEENV 180
 DB 121 AELEGGTSSLANTNNKNWVLSGFQHGDAFTRWLKIPEKNKIIILIGIDWTDTEENV 180
 QY 181 IPGRYINLTYKTEBAGWLAGYANASFLAKKPSDPTKRSALVIGGGSIPAVTDFIAGYL 240
 DB 181 IPGRYINLTYKTEBAGWLAGYANASFLAKKPSDPTKRSALVIGGGSIPAVTDFIAGYL 240
 QY 241 AGIKAWNLKNSDKKTKITTDKIEINLGFVDQSTKERLEQIASKDKPSTLLAVAGPLTE 300
 DB 241 AGIKAWNLKNSDKKTKITTDKIEINLGFVDQSTKERLEQIASKDKPSTLLAVAGPLTE 300
 QY 301 IFSDIIANQNDRYLIGVTDQSLVYTKTKNKFPTSIILKNLGYSVFSVLSDLYTKKSNSRN 360

Db 301 IFSDIIANGDRYLIGVDTQSLVYTKTKKFFSILKNLGYSVFSLDLYTKKSNRN 360
 Qy 361 LAEPFGKSAATYVGLGKDRPVDIADTSLSGNDKKLATEAISEAKKEFEKTKTIPAEV 420
 Db 361 LAEPFGKSAATYVGLGKDRPVDIADTSLSGNDKKLATEAISEAKKEFEKTKTIPAEV 420
 Qy 421 RKTLEIPEMPDKOPDKQESLDKLITDINKN 451
 Db 421 RKTLEIPEMPDKOPDKQESLDKLITDINKN 451

RESULT 3

AA015862

ID AA015862 standard; protein: 423 AA.

AC AA015862;

DT 16-JAN-2003 (first entry)

XX Mutant Mycoplasma hyopneumoniae mhp3 protein.

XX Apoprotein antigen; enzootic mycoplasma pneumonia; mhp3; mutant; mutein;
 KM vaccine; Mycoplasma hyopneumoniae infection.

XX Mycoplasma hyopneumoniae.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 70 /note= "Encoded by RGT"

FT Misc-difference 422 /note= "Wild type Lys replaced by Asn"

FT Misc-difference 423 /note= "Wild type Asn replaced by Leu"
 FT EP1245677-A1.

XX 02-OCT-2002.
 XX 30-MAR-2001; 2001EP-00303030.
 XX 30-MAR-2001; 2001EP-00303030.

XX (PFIZ) PFIZER PROD INC.
 XX King KM, Madura RA, Rosey EL;
 XX WPI; 2002-742716/81.
 XX N-PSDB; AAL50633.

XX Novel apoprotein antigens encoded by Mycoplasma hyopneumoniae for use in
 PT vaccines to prevent and treat diseases caused by infection with
 PT Mycoplasma hyopneumoniae in animals, especially pigs.
 XX Claim 4; Page 20-21; 38pp; English.

XX The invention comprises the amino acid and coding sequences of Mycoplasma
 CC hyopneumoniae mhp3 proteins, the invention also comprises novel
 CC apoprotein antigens encoded by the M. hyopneumoniae mhp3 gene. M.
 CC hyopneumoniae is a bacterial pathogen that causes enzootic mycoplasma
 CC pneumonia in pigs. The mhp3 genes, proteins and apoprotein antigens of
 CC the invention are useful in the manufacture of a vaccine for treating/
 CC preventing a disease or disorder caused by infection with M.
 CC hyopneumoniae in an animal, especially a pig. The present amino acid
 CC sequence represents a mutant version of the Mycoplasma hyopneumoniae mhp3
 CC protein which was modified for expression in E. coli

XX Sequence 423 AA;

Query Match 92.8%; Score 2134; DB 5; Length 423;
 Best Local Similarity 99.8%; Pred. No. 3,4e-152;
 Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 30 MDKETTKEEKADNONKQITDVSKIISGLVNERKSEIIPAAKADANKHGLMMAIVTAGTV 89
 Db 2 MDKETTKEEKADNONKQITDVSKIISGLVNERKSEIIPAAKADANKHGLMMAIVTAGTV 61
 Qy 90 NDNSFNQSSWEAIIQGLALTGSEITVSSTAELEGKSSSLANTNNKVVWLSGFQHDAP 149
 Db 62 NDNSFNQSSWEAIIQGLALTGSEITVSSTAELEGKSSSLANTNNKVVWLSGFQHDAP 121
 Qy 150 TRWLKIPENKQLETKNIIILGIDMTDENVIPTGRYINLTYTEAGWLAGVANASFLA 209
 Db 122 TRWLKIPENKQLETKNIIILGIDMTDENVIPTGRYINLTYTEAGWLAGVANASFLA 181
 Qy 210 KKEPSPDPTKSAIIVIGGISPATVDPIAGYIAGIKAMNLSNPKTKITTDKIEINLQFD 269
 Db 182 KKEPSPDPTKSAIIVIGGISPATVDPIAGYIAGIKAMNLSNPKTKITTDKIEINLQFD 241
 Qy 270 VDDSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANGNDRYLIGVDTQSLVYTKTK 329
 Db 242 VDDSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANGNDRYLIGVDTQSLVYTKTK 301
 Qy 330 NKEPFTSLKNLGYSVFSLDLYTKKSNRNLAGFEFGKSAATYVGLGKDRPVDIADTSL 389
 Db 302 NKEPFTSLKNLGYSVFSLDLYTKKSNRNLAGFEFGKSAATYVGLGKDRPVDIADTSL 361
 Qy 390 EGNDDKLATEAISEAKKEFEKTKTIPAEVRKTLIEIPMPDKOPDKQESLDKLITDIN 449
 Db 362 EGNDDKLATEAISEAKKEFEKTKTIPAEVRKTLIEIPMPDKOPDKQESLDKLITDIN 421

RESULT 4

AAU01860

ID AAU01860 standard; protein: 423 AA.

AC AAU01860;

DT 07-SEP-2001 (first entry)

XX Mycoplasma hyopneumoniae recombinant MHP3 antigen.

XX MHP3; antigen; vaccine; enzootic mycoplasma pneumonia; mutant; antibody;
 KM immunosassay; immunotherapy; anti-idiotypic antibody; mutein.

XX Mycoplasma hyopneumoniae.

FH Key Location/Qualifiers

FT Misc-difference 70 /note= "Encoded by RGA"

FT Misc-difference 417..422 /note= "Encoded by AATTACCGATAT"
 XX EP1090995-A2.

XX 11-APR-2001.
 XX 26-SEP-2000; 2000EP-00308421.

XX 29-SEP-1999; 99US-0156602P.
 XX (PFIZ) PFIZER PROD INC.

XX King KM, Madura RA, Rosey EL;
 XX WPI; 2001-309781/33.
 XX N-PSDB; AAS03286.

XX New apoprotein antigens encoded by mhp3 gene from Mycoplasma
 PT hyopneumoniae useful as a vaccine for treating or preventing diseases
 PT caused by Mycoplasma hyopneumoniae.

XX Claim 4; Page 19-21; 38pp; English.

The sequence represents Mycoplasma hyopneumoniae a recombinant MHP3

CC antigen lacking the first 28 amino acids (the putative signal sequence).
CC MHP3 antigen and its fragments are useful in manufacturing a vaccine for
CC treating or preventing a disease or disorder in an animal, especially
CC pig, caused by M. hyopneumoniae infection e.g. enzootic mycoplasma
CC pneumonia. The mhp3-encoded proteins may be used as immunogens to
CC generate antibodies which immunospecifically bind such an immunogen. The
CC antibodies generated against the antigen are useful in diagnostic
CC immunoassays, passive immunotherapy and generation of anti-idiotypic
CC antibodies. Mhp3 proteins may also be used in immunoassays, e.g. to
CC detect or measure in a biological sample from a vaccinated or potentially
CC infected test animal the presence of antibodies to the antigen, and thus
CC to monitor the immune response and/or to diagnose infection of the animal
XX
SQ Sequence 423 AA;
Query Match 91.7%; Score 2109; DB 4; Length 423;
Best Local Similarity 99.8%; Pred. No. 2.6e-150;
Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 30 WDKETTKEEKSADNQNQITDVSKISGLVNERKSEIMAKADANKHFGMAIVTAGGTV 89
DB 2 WDKETTKEEKSADNQNQITDVSKISGLVNERKSEIMAKADANKHFGMAIVTAGGTV 61
QY 90 NDNSFNQSGWEAIIQOLGALTGGEITVSVDSTAELEBKTSILANTYKXWVLSGFQHGDAF 149
DB 62 NDNSFNQSGWEAIIQOLGALTGGEITVSVDSTAELEBKTSILANTYKXWVLSGFQHGDAF 121
QY 150 TRWLKIPENKOLFTEKNIIIGIDMTDENVIPTGRYINLTGYKTEBEAGMLAGYANASPIA 209
DB 122 TRWLKIPENKOLFTEKNIIIGIDMTDENVIPTGRYINLTGYKTEBEAGMLAGYANASPIA 181
QY 210 KKPSDPTKSAIYIGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINIGFD 269
DB 182 KKPSDPTKSAIYIGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINIGFD 241
QY 270 VQDSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIINQNDRLIIGVDTQSLVYTTKX 329
DB 242 VQDSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIINQNDRLIIGVDTQSLVYTTKX 301
QY 330 NKFTSILKNLGYSVFSLDLYTKKNSRMLAGPEFKSATYVYLGIKDRFVIDIADTSL 389
DB 302 NKFTSILKNLGYSVFSLDLYTKKNSRMLAGPEFKSATYVYLGIKDRFVIDIADTSL 361
QY 390 EGNDKLATEAISEAKKEFEKTKTIPAEVRYKTLIEIPMDPKQPDQOESLIDKL 444
DB 362 EGNDKLATEAISEAKKEFEKTKTIPAEVRYKTLIEIPMDPKQPDQOESLIDKL 416
RESULT 5
AAR40856
ID AAR40856 standard; protein; 453 AA.
XX
AC AAR40856;
XX
DT 25-MAR-2003 (revised)
DT 07-MAR-1994 (first entry)
XX
DE 43kd regression associated antigen.
XX
KW Regression associated antigen; tumour; immunotherapy;
KM anti-idiotypic antibodies; antibodies; tumour regression.
XX
OS Mycoplasma hyorhinis.
FH Key Location/Qualifiers
FT Misc-difference 80 /note= "Tryptophan encoded by TGA, normal in Mycoplasma
FT /note= "Tryptophan encoded by TGA, normal in Mycoplasma
FT Misc-difference 124 /note= "Tryptophan encoded by TGA, normal in Mycoplasma
FT /note= "Tryptophan encoded by TGA, normal in Mycoplasma
FT Misc-difference 165 /note= "Tryptophan encoded by TGA, normal in Mycoplasma
FT

FT
FT Misc-difference 344 /note= "Tryptophan encoded by TGA, normal in Mycoplasma
FT /note= "Tryptophan encoded by TGA, normal in Mycoplasma
FT
XX
XX US5242823-A.
XX
XX 07-SEP-1993.
XX
XX 02-OCT-1992; 92US-00956546.
XX
XX 07-MAR-1986; 86US-00837494.
XX 16-SEP-1987; 87US-00097910.
XX 11-DEC-1987; 87US-00131815.
XX 04-JAN-1988; 88US-00138923.
XX 16-MAR-1990; 90US-00474730.
XX
XX (IRGE-) INT GENETIC ENG INC.
XX
XX Fareed GC, Sen A, Ghosh-Dastidar P, Jar-How L;
XX
XX WPI; 1993-295229/37.
XX
XX N-PSDB; AAQ47816.
XX
XX DNA encoding a regression-associated antigen from M. hyorhinis - is used
XX to obtain prods. for diagnosis, localisation and therapy of tumours.
XX
XX Disclosure; Fig 3; 40pp; English.
XX
XX Regression associated antigens (RAA's) are identified in material from
XX neoplastic cells by their immunological reactivity with regression
XX associated antibodies from the serum of patients diagnosed as undergoing
XX regression of a tumour. RAA's can be used for tumour immunotherapy and
XX for producing and purifying antibodies which can be used for tumour
XX diagnosis, localisation and therapy. The antibodies can also be used for
XX the production of anti-idiotypic antibodies which can also be used in
XX immunotherapy. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 453 AA;
Query Match 31.1%; Score 714.5; DB 2; Length 453;
Best Local Similarity 38.2%; Pred. No. 3.5e-45;
Matches 175; Conservative 86; Mismatches 150; Indels 45; Gaps 16;
QY 14 GLVPELSAAT-ISAGCMDEKTKEEKSADNQNQITDVSKISGLVNERKSEIMAKADA 72
DB 12 GTISTVASVATFVSCG---ETDKGKII-----RIPD-----NSFVADROAEIRKA----- 54
QY 73 NKHFGMLMAIVTAGGTINDNSFNQSGWEAIIQOLGALTG-GEITVSVDSTAELEBK 127
DB 55 -KNDFEFTVLLTAGGTIVQDKSFNQSWEAVLEHYDQIEKTNLDRAVQETNNQSELIGKY 113
QY 128 SSLANTKNVWVLSGFQHGDAFTRWLKIPEH-----KOLFTEKNIIIGIDM--TPTEN 179
DB 114 KNFLNGKNKWVILTFQGGQGFPEFKLQKOTDSNGKKYSDLLAEKVIIVAVDMDSKEDKO 173
QY 180 VIPTGRYINLTGYKTEBEAGMLAGYANASFLAKKPSDPTKSAIYIGGISPAVTDFIAGY 239
DB 174 LKAGHPTSLYKTEBEAGFLIAGVASKFLAYKFPNDKAKRTIAPFGGHHGAVTDFIAGF 233
QY 240 LAGIKAWNLKNSDKKTKITTDKIEINIGFVQDSTKERLEQIASKDKPSTLLAVAGPLT 299
DB 234 LAGIAKANNNDNPTAKVITISDNNINIDPGF-ISNDKTFPTINGVYKNS-SLIVLPVGSLSLT 290
QY 300 EIFSDII--ANQNDRYLIGVDTQSLVYTTKKNKFFTSILKNLGYSVFSLDLYTKKSN 357
DB 291 SSVVDAIKKSKDKTKYLIGVDTQSKIFPPA-TYFFTSIEKHLAKRTIYEVLITDILWKED 349
QY 358 SRNLAGEFPGK---KSATVYLGIKDRFVIDIADTSLGNDKRLATEAISEAKKEFEKTKX 413
DB 350 SKFLGSFRSPFLTNPNATATYKGISDPSGVSNSTVADADKVKYKQEFLEATADAFKQIQ 409
QY 414 TIPAEVRYKTLIEIPMD--PKQPDQOESLIDKLITDIN 449

Db 410 ANPT-NYKSVLGIPPTMLINDNDADAKNEKALNELIKIN 446

RESULT 6

AAO15867 standard; protein; 457 AA.

AAO15867;

16-JAN-2003 (first entry)

Mycoplasma hyorhinis Ag234-5 protein.

Apoptocin antigen; enzootic mycoplasma pneumoniae; mhp3; Ag234-5;

Mycoplasma hyorhinis.

EP1245677-A1.

02-OCT-2002.

30-MAR-2001; 2001EP-00303030.

30-MAR-2001; 2001EP-00303030.

(PRIZ) PRIZER PROD INC.

King KW, Madura RA, Rosey EL;

WPI; 2002-742716/81.

Novel apoptocin antigens encoded by Mycoplasma hyopneumoniae for use in vaccines to prevent and treat diseases caused by infection with Mycoplasma hyopneumoniae in animals, especially pigs.

Example; Fig 1; 38pp; English.

The invention comprises the amino acid and coding sequences of Mycoplasma hyopneumoniae mhp3 proteins, the invention also comprises novel apoptocin antigens encoded by the M. hyopneumoniae mhp3 gene. M. hyopneumoniae is a bacterial pathogen that causes enzootic mycoplasma pneumonia in pigs. The mhp3 genes, proteins and apoptocin antigens of the invention are useful in the manufacture of a vaccine for treating/preventing a disease or disorder caused by infection with M. hyopneumoniae in an animal, especially a pig. The present amino acid sequence represents the Mycoplasma hyorhinis Ag234-5 protein which is shown in a figure of the invention

Sequence 457 AA:

Query Match 30.7%; Score 706; DB 5; Length 457;

Best Local Similarity 38.4%; Pred. No. 1.5e-44;

Matches 173; Conservative 87; Mismatches 145; Indels 46; Gaps 16;

14 GLVPEPLAIAAT-ISAQCMDEKTEKESADNONQITDVSKISGLVNERKSEIMAAKADA 72

12 GTISTVASVATFVSCG---ETDREGKTI---RIFP---NSFVKDRQAEIERA--- 54

73 NKHFGMLMAIYTAGTVDNSFNQSSWEAI-----QQLGALTG-GEITVSDSTALEBGKY 127

55 -KNDFPNTVLITAGTVDKSFNQSIMEVALEHVDQIEKTNLDRVSETNNGSELIGKY 113

128 SSLANTKNVAVSGFQHGDAFTWMLKIPEN-----KQLFTEKNIILGIDW---TDTEN 179

114 KNPLNGKNKVMILTGFOGGEFPKFLKQTDNSNGKYSDDLAEKVVIIYAVVMDLSKEDKD 173

180 VIPLGRYNTLYKTEBEAGMLGAVANASFLAKKPSDPFKRSAYIVGGISPAVTDFTAGY 239

174 LTKKHGHSLLYKTEBEAGMLGAVANASFLAKKPSDPFKRSAYIVGGISPAVTDFTAGY 233

240 LAGIKAVNLKNSDKTKITTDKIEINLGFVDQDSTKERLEQIASKDKPSTLLAVAGPLT 299

Db 234 LAGIAKTNNDNPTAKVITSDNNINIDYGF-ISNDKATPFIINGIVNKS--SLVLPVAGSLT 290

Qy 300 EIFSDII--ANQNRVYLGVDTOGSLVYTKKNEFTSILKNLGVSFVSVDLYTKSN 357

Db 291 SSVVDALKNSKDKTKYILGVDTQSKIFSPA-TVFFTSIEHGLRRTYQVLTIDMLKED 349

Qy 358 SRNLAGEFPGK---KSAFVYLGIDRFVDIADTSLGNDKKLATEAISEAKKEFEKTK 413

Db 350 SKFLGSFRSPFLTNPAATYKKGISDDFVGVSNTVADADKVKRQEFLEATADFKKIQ 409

Qy 414 TIPAEVRKTLIEIPW---PDKOPDKOESL 441

Db 410 ANPT-NYKSVLGIPPTMLINDNDADAKNEKASL 439

RESULT 7

AA67582 standard; protein; 432 AA.

AA67582;

06-OCT-1995 (first entry)

Cancer metastasis protein.

Cancer metastasis; clinical tests; detection.

Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 55 /note= "corresponding codon TGA"

FT Misc-difference 99 /note= "corresponding codon TGA"

FT Misc-difference 140 /note= "corresponding codon TGA"

FT Misc-difference 319 /note= "corresponding codon TGA"

FT Misc-difference 420 /note= "corresponding codon TGA"

FT Misc-difference 424 /note= "corresponding codon TGA"

PN JP06319559-A.

PD 22-NOV-1994.

PF 12-MAY-1993; 93JP-00144165.

PR 12-MAY-1993; 93JP-00144165.

PA (HAYB) HAYASHIBARA SEIBUTSU KAKAKU.

DR WPI; 1995-040317/06.

DR N-PSDB; AAQ79124.

FT DNA encoding polypeptide involved in cancer metastasis - useful for the study of the mechanism of metastasis and in clinical tests.

PS Claim 1; Page 2; Japanese.

CC AAQ79124 encodes AA67582 a protein involved in cancer metastasis, which may be used for the study of metastatic mechanisms, and for clinical tests to determine the presence or absence of cancer metastasis

CC Sequence 432 AA;

Query Match 30.2%; Score 694.5; DB 2; Length 432;

Best Local Similarity 39.0%; Pred. No. 1.1e-43;

Matches 168; Conservative 81; Mismatches 141; Indels 41; Gaps 14;

Qy 33 ETTKEKSDNONQITDVSKISGLVNERKSEIMAAKADAKHFGMLMAIYTAGTVDND 92

```
Db 3 ETDKGGKII-----RIFD-----NSFVKDRQAEIEKA-----KNDFENVLLTAGGTVDK 48
Qy 93 SFNOSWEAI-----QOLGALTG-GEITSVDSSTAIEGKYSILANTKNWVWLSGFQHD 147
Db 49 SFNOSIWEAVLEHYDQIEKTTNLDKRVSOETNNOSBLIKYKFNKGNKWNVLIGFQGG 108
Qy 148 AFTEMLKIPEN-----KOLFTEKNIILIGIDW---TDTEENVIPGRYINLTYTEEAGWL 199
Db 109 EFPFELKQTDNSNGKKYSDLLAEKKVILIVAVDMDSKEDKDLIKKHGFIISLYKTEEAGFI 168
Qy 200 AGYANASFLAKKPSDPTKRSALIVGGISPAVYDFIAGYIAGIKANLKNSSDKTKTTT 259
Db 169 AGYASSKFLAYKFPDEAKRTIAPFGGHHGAGVDFIAGIAGIAYKNNNDPTGCVTISD 228
Qy 260 DKIEINLGFVDYDSTKERLEQIASKDKPSTLLAVAGLTFESDII--ANONDRYLIGV 317
Db 229 NNINIDTGF-ISNDKTATFINGIYNKS--SLVLPVAGSLTSSVDALKSNKDTKYLIGV 285
Qy 318 DTDQSLVYTKTKNKFSTILKNLGYSVFSLDLYTKKSNRNLAGFEFGK---KSATV 373
Db 286 DTDQSKIFSPA-TVFFTSIEKHLGRTIYQVLDIWLKEDSKFLGSFSLTNPANATV 344
Qy 374 YLGKDRFVDIADTSLSGNDKKLATEAISEAKKEFEKTKTIPEAEVAKTLEIPEM--P 430
Db 345 YKGISDPEVGVNSNTVADADKVKAKQEFINEATADFKKOIQANPT-NYKSVLGIPMTLIND 403
Qy 431 DKOPDKOESL 441
Db 404 NDAKONEKASL 414
```

```
RESULT 8
AAP93343
ID AAP93343 standard; protein; 448 AA.
AC AAP93343;
XX 25-MAR-2003 (revised)
DT 01-AUG-1990 (first entry)
XX
DE Gene encoding the 43 kd regression-associated antigen (RA Ag) of
DE Mycoplasma hyorhinis.
XX
KW Tumour regression-associated antigens (RA Ag); in vivo imaging;
KW therapy monitoring; cancer therapy; Mycoplasma hyorhinis.
XX
OS Mycoplasma hyorhinis.
XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT Protein 26..448
XX
PN EP308265-A.
XX
XX 22-MAR-1989.
XX
XX 16-SEP-1988; 88EP-00308625.
XX
XX 16-SEP-1987; 87US-00097910.
XX
XX 11-DEC-1987; 87US-00131815.
XX
XX (ITGE-) INT GENETIC ENG INC.
XX (INGE-) INGENE INT GENETIC.
XX (INGE-) INGENE INT GENETIC.
XX
PI Fareed GC, Sen A, Ghoshdasti P, Li A, Lee JH;
XX
XX WPI; 1989-087638/12.
XX
XX N-PSDB; AAN90684.
XX
XX Tumour regression-associated antigens and antibodies - used in diagnostic
XX tests, monitoring course of therapy and for therapy in cancer patients.
XX
XX
```

```
XX
PS Disclosure; Page 7; 56pp; English.
XX
CC Regression-associated antigens may be used in diagnostic tests, eg in
CC vivo imaging, for monitoring the course of therapy or for therapeutic
CC purposes, eg active immunisation protocols in cancer patients or drug
CC delivery systems by binding the drug to monoclonal or monospecific
CC polyclonal Ab showing specific immunoreactivity with the Ag. (Updated on
CC 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
SQ Sequence 448 AA;
```

```
Query Match 28.5%; Score 655; DB 1; Length 448;
Best Local Similarity 37.4%; Pred. No. 1e-40;
Matches 171; Conservative 89; Mismatches 149; Indels 48; Gaps 20;

Qy 14 GLVFPPLAIAT-ISAQMDKETTKEESADNONKQITDVSKISLVNERKSEIIMAAADA 72
Db 12 GTISTVASVATFVSCG-----ETDKGGKII-----RIFD-----NSFVKDRQAEIEKA----- 54
Qy 73 NKHFGMLMAIYTAGTVDNSFNOSWEAI-----QOLGALTG-GEITSVDSSTAIEGKY 127
Db 55 -KNDFENVLLTAGGTVDKXSFNOSIWEAVLEHYDQIEKTTNLDKRVSOETNNOSBLIKY 113
Qy 128 SSLANTKNWVWLSGFQHDGDAFTKMLKIPEN-----KOLFTEKNIILIGIDW---TDTEN 179
Db 114 KNFLNGKNWVWILIGFQGGQGFPRFLKQTDNSNGKKYSDLLAEKKVILIVAVDMDSKEDKD 173
Qy 180 VIPGRYINLTYTEEAGMLAGYANASFLAKKPSDPTKRSALIVGGISPAVYDFIAGY 239
Db 174 LKAGHFISLYKTEEAGFIAGYASSKFLAYKFPDEAKRTIAPFGGHHGAGVDFIAGF 233
Qy 240 LAGIKANNLKNSSDKTKITTDKIEINLGFVDYDSTKERLEQIASKDKPSTLLAVAGPLT 299
Db 234 LAGIAKTNNDNPTAKVTISDNINIDTGF-ISNDKTATFINGIYNKS--SLVLPVAGSLT 290
Qy 300 EIFSDII--ANONDRYLIGVDTQSLVYTKNKFSTILKNLGYSVFSLDLYTKSN 357
Db 291 SSVVDALIKSNKDKTYLIGVDTQSKIFSPA-TVFFT-IEKHLGRTIYEVLDIWLKED 348
Qy 358 SRNLAGFEFGK---KSATYIYLGKDRFVDIADTSLSGNDKKLATEAISEAKKEFEKTK 413
Db 349 S-FLGSFRSPFLTNAANAATYKGISD-FLGSNSTVADADKVKAKQEFIN-ATADFKKQIQ 405
Qy 414 TTPAEVAKTLEIPEM--PDKQPDKQESLDKLTINDIN 449
Db 406 ANPT-NYKSVLGIPMTLINDNDAKNEKALNELIKIN 441

RESULT 9
AA05332
ID AA05332 standard; peptide; 428 AA.
AC AA05332;
XX
XX 25-JUN-1999 (first entry)
XX
XX Inflammatory cytokine inducer.
XX
XX Inflammatory cytokine inducer; thrombocytopenia; therapy.
XX
XX Synthetic.
XX
XX JP11089582-A.
XX
XX 06-APR-1999.
XX
XX 19-SEP-1997; 97JP-00273649.
XX
XX 19-SEP-1997; 97JP-00273649.
XX
XX (CHUS ) CHUGAI PHARM CO LTD.
```

XX WPI; 1999-281057/24.
 DR N-PSDB; AAX33847.
 XX New inflammatory cytokine inducer gene and polypeptide - useful for
 PT treatment of thrombocytopenia.
 XX
 XX Claim 3; Page 16-17; 22pp; Japanese.
 XX
 CC This sequence represents the inflammatory cytokine of the invention. The
 CC inflammatory cytokine can be used in a drug, which is useful for the
 CC treatment of thrombocytopenia
 CC
 CC
 SQ Sequence 428 AA;
 Query Match 17.2%; Score 394.5; DB 2; Length 428;
 Best Local Similarity 26.8%; Pred. No. 4.2e-21;
 Matches 126; Conservative 101; Mismatches 174; Indels 69; Gaps 20;
 QY 5 IKNNKFLGLVPLSAI-ATISAGCWDEKTEKESADNQNKOITDVSIGLVNERKS 63
 DB 1 MKSKSKILLGL-SPAILPRAVAVSCGNDES-----NISPEKDISKTTTNANGKQ 52
 QY 64 EIMAAKADANKHGLNMAIYTAGTVNDNSFNQSSWEAIOQLALTGCEITSVDSTAE 123
 DB 53 VVKNAL- -LKLKPVLLTDEGKIDKSPNOSAFALAIKQIGIEINNVPS-SNF 106
 QY 124 EGKYSILANTNNKVVVLSGFQHGDAFTRWLKIPEKNKOLFTEKNIIILIGIMDTOTENVIPT 183
 DB 107 ESAVNSALSGHKIWIWNGFRKHOOSIKQY--IDAHRELERNOIKIIGIDF-DIETEKW 163
 QY 184 GRVINTLYKTEAGWLAGVANASFLAKKPPSDPTKRSATVIYGGISPAVDFIAGYLAGI 243
 DB 164 --FYSIQFNKESAFITGVALIASWLSQ--DESKRVASFGGAFGVITTFNNGFAKGI 218
 QY 244 KANWLKNSDKTKTI-TTDKIEINLGFVODSTKERLEQIAS-----KDKPESTL 292
 DB 219 LYYNQKH--KSSKIYHNSPVKLDGCF-----TAGKKNVTYINNVLSSTPADVKKNPVIL 271
 QY 293 AVAGPLTEIRSDIINANDRYLIGVDTQSLVYTKTKNKFETSLKVLGYSVFSVLSDL- 351
 DB 272 SVAGPAT--FETVRLANKGVYIGVSDQGM1--QDDRLITSLVKIKQAVVETLLDLI 327
 QY 352 -----YTKSNSNRLAGFEFGKKSATVIYLGIKDRFVDIADTSLGNDKDL-ATEAI 401
 DB 328 LEKEEGKPVYVYKDKADKTKSHFGTO-----KKKMGVAAHNSNTEBQAKINNKI 379
 QY 402 SEAKKEFEKTKTIPAEVRKTLIEIPMPD-KQPKQOESLDKLITDINK 450
 DB 380 KEAIIKMFKE---LPEDFVKYINSDKALKQGNKIDNVSERLEAIIISAINK 425
 RESULT 10
 ABP71709
 ID ABP71709 standard; protein; 428 AA.
 XX
 AC ABP71709;
 XX
 DT 04-APR-2003 (first entry)
 XX
 DE M161 antigen amino acid sequence.
 XX
 KM M161; antigen: cytotoxic T-lymphocyte inducer; CTL; cytostatic; cancer;
 KM anticancer agent.
 XX
 OS Mycoplasma fermentans.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 121 /note= "Encoded by TGA; unexplained stop codon in coding
 FT sequence"
 FT Misc-difference 163 /note= "Encoded by TGA; unexplained stop codon in coding
 FT sequence"
 FT Misc-difference 163 /note= "Encoded by TGA; unexplained stop codon in coding
 FT sequence"

FT sequence"
 FT Misc-difference 185 /note= "Encoded by TGA; unexplained stop codon in coding
 FT sequence"
 FT Misc-difference 348 /note= "Encoded by TGA; unexplained stop codon in coding
 FT sequence"
 FT Misc-difference 358 /note= "Encoded by TGA; unexplained stop codon in coding
 FT sequence"
 FT WO2002102402-A1.
 PN 27-DEC-2002.
 PD 13-JUN-2002; 2002WO-JP005916.
 PF 15-JUN-2001; 2001JP-00182250.
 PR (TAKE) TAKEDA CHEM IND LTD.
 PA Seya T, Matsumoto M, Naito K;
 PI WPI; 2003-167451/16.
 DR N-PSDB; ABZ59715.
 XX
 XX M161 antigen, its peptide fragment or their salt with e.g. superior CTL-
 PT inductive effect, applicable in anticancer agents combined with cancer
 PT antigen for preventing or treating cancer.
 XX
 XX Disclosure; Fig 1; 94pp; Japanese.
 PS
 XX The invention relates to cytotoxic T-lymphocyte (CTL)-inducers containing
 CC the M161 antigen, its partial peptide or their salt. The activity of CTL-
 CC inducers of the invention may be described as cytostatic. The antigen or
 CC its peptide fragment are applicable in anticancer agents for the
 CC prevention or treatment of cancer. The antigen and its derivative have
 CC superior CTL-inductive effect, giving anticancer agents that have low
 CC toxicity. The current sequence represents the M161 antigen amino acid
 CC sequence
 SQ Sequence 428 AA;
 Query Match 17.2%; Score 394.5; DB 6; Length 428;
 Best Local Similarity 26.8%; Pred. No. 4.2e-21;
 Matches 126; Conservative 101; Mismatches 174; Indels 69; Gaps 20;
 QY 5 IKNNKFLGLVPLSAI-ATISAGCWDEKTEKESADNQNKOITDVSIGLVNERKS 63
 DB 1 MKSKSKILLGL-SPAILPRAVAVSCGNDES-----NISPEKDISKTTTNANGKQ 52
 QY 64 EIMAAKADANKHGLNMAIYTAGTVNDNSFNQSSWEAIOQLALTGCEITSVDSTAE 123
 DB 53 VVKNAL- -LKLKPVLLTDEGKIDKSPNOSAFALAIKQIGIEINNVPS-SNF 106
 QY 124 EGKYSILANTNNKVVVLSGFQHGDAFTRWLKIPEKNKOLFTEKNIIILIGIMDTOTENVIPT 183
 DB 107 ESAVNSALSGHKIWIWNGFRKHOOSIKQY--IDAHRELERNOIKIIGIDF-DIETEKW 163
 QY 184 GRVINTLYKTEAGWLAGVANASFLAKKPPSDPTKRSATVIYGGISPAVDFIAGYLAGI 243
 DB 164 --FYSIQFNKESAFITGVALIASWLSQ--DESKRVASFGGAFGVITTFNNGFAKGI 218
 QY 244 KANWLKNSDKTKTI-TTDKIEINLGFVODSTKERLEQIAS-----KDKPESTL 292
 DB 219 LYYNQKH--KSSKIYHNSPVKLDGCF-----TAGKKNVTYINNVLSSTPADVKKNPVIL 271
 QY 293 AVAGPLTEIRSDIINANDRYLIGVDTQSLVYTKTKNKFETSLKVLGYSVFSVLSDL- 351
 DB 272 SVAGPAT--FETVRLANKGVYIGVSDQGM1--QDDRLITSLVKIKQAVVETLLDLI 327
 QY 352 -----YTKSNSNRLAGFEFGKKSATVIYLGIKDRFVDIADTSLGNDKDL-ATEAI 401

Db 328 LEKEGGYPVYVKDKADKMSHFQTQ-----KEKWIGVAAENHFSNTEEQAKINNKI 379
Qy 402 SEAKKEFEKTKTIPAEVEKRTLEIPMPD-KQPDQOESLDKLTIDINK 450
Db 380 KEAIKMFKE----LPEDFVKYINDKALKDGNKIDNVSERLEAIIISAINK 425

RESULT 11
ADK68531
ID ADK68531 standard; protein; 428 AA.
XX
AC ADK68531;
XX
DT 06-MAY-2004 (first entry)
XX
DE Mycoplasma fermentans IL-X precursor protein #1.
XX
KM Immunoregulatory factor; IL-X; lymphocyte proliferation.
XX
OS Mycoplasma fermentans.
XX
FH Key location/Qualifiers
FT Peptide 1..24
FT /label= Signal_peptide
FT Protein 25..428
FT /note= "Mature IL-X protein"

US6506892-B1.
XX
PD 14-JAN-2003.
XX
PE 29-OCT-1998; 98US-00182625.
XX
PR 29-OCT-1997; 97US-0063701P.
XX
PA (WEBB/) WEBB A C.
XX PA (BLAZ/) BLAZAR B A.
XX
PI Webb AC, Blazar BA;
XX
XX WPI: 2003-401108/38.
DR N-PSDB; ADK68530.
XX
XX New isolated polynucleotide, useful for augmenting proliferation of B and T lymphocytes.
XX
PS Claim 25; SEQ ID NO 9; 42pp; English.
XX
CC The invention provides novel immunoregulatory factor designated IL-X
CC which has been isolated Mycoplasma and polynucleotides encoding such
CC polypeptides. The polynucleotide is useful for augmenting proliferation
CC of B and T lymphocytes. The present sequence is Mycoplasma fermentans IL-
CC X precursor protein.
XX
XX Sequence 428 AA;

Query Match 17.1%; Score 393.5; DB 7; Length 428;
Best Local Similarity 26.8%; Pred. No. 5e-21;
Matches 126; Conservative 101; Mismatches 174; Indels 69; Gaps 20;

Qy 5 IKNNKFTLGLGVFPLISAI-ATISAGCWDKETTKEBKADNONKQITDVSKISGLVNERKS 63
Db 1 MKSKSKTILGL-SPIAAILPVAVSCGNNDSE-----NISFKKDISKYTTTANQKQ 52
Qy 64 EIMAKAKDANHFPGINMAIVTAGTVNDNSFNQSWEAIOGLALTGGEIITSVDSSTAEL 123
Db 53 VVKQAEI-----LKLKPYLITDEGKIDKSFNQSFEALKAINKQTGIEINNVEPS-SNF 106
Qy 124 EGYTSLANTNKNNVWVLSGFQHGDAFTRMKIPENKQIFTEKNIIILGIDWTDTEENVIPT 183
Db 107 ESAVNSALMSAGHKIIVNLGFKHQOSIKQY--IDAHRLELNQIKIITIDF-DIETEKW 163
Qy 184 GRVYNLYTKTEAGWLAGYANASFLAKKPPSDPTKRSIVIGGIGSPAVTDIAGYLAGI 243

Db 164 --FYSIQFNIKESAFITGVAIASWLSQ---DESKRVVASFGGAFPGVTFPEGFAKGI 218
Qy 244 KAMVLKNSDKKTKI-TTDKIEINLGFVODPTSTKERLEQIAS-----KDKPSTLL 292
Db 219 LYINQKG--KSSKIYHSPVKLDSGF-----TAGERKNYIINNVLSTPADVKKNPVIL 271
Qy 293 AVAGPLTEIFSDIILANONRYLIGVDTQSLVYTKTKNKKFPTSLKNLGSVPSVLSDL- 351
Db 272 SVAGPAT--FEYVLANKGVIGVDSDDQMI--QDKDRILTSVLKHIKQAVETLLDLI 327
Qy 352 -----YTKSNSNINLAFERFGKSAIVYLGIKDRFVDIADTSLSGNDKXL-ATEAI 401
Db 328 LEKEGGYPVYVKDKADKMSHFQTQ-----KEKWIGVAAENHFSNTEEQAKINNKI 379

Qy 402 SEAKKEFEKTKTIPAEVEKRTLEIPMPD-KQPDQOESLDKLTIDINK 450
Db 380 KEAIKMFKE----LPEDFVKYINDKALKDGNKIDNVSERLEAIIISAINK 425

RESULT 12
ADK68538
ID ADK68538 standard; protein; 428 AA.
XX
AC ADK68538;
XX
DT 06-MAY-2004 (first entry)
XX
DE Mycoplasma fermentans IL-X precursor protein #2.
XX
KM Immunoregulatory factor; IL-X; lymphocyte proliferation.
XX
OS Mycoplasma fermentans.
XX
FH Key location/Qualifiers
FT Peptide 1..24
FT /label= Signal_peptide
FT Protein 25..428
FT /note= "Mature IL-X protein"

US6506892-B1.
XX
PD 14-JAN-2003.
XX
PE 29-OCT-1998; 98US-00182625.
XX
PR 29-OCT-1997; 97US-0063701P.
XX
PA (WEBB/) WEBB A C.
XX PA (BLAZ/) BLAZAR B A.
XX
PI Webb AC, Blazar BA;
XX
XX WPI: 2003-401108/38.
DR N-PSDB; ADK68535.
XX
XX New isolated polynucleotide, useful for augmenting proliferation of B and T lymphocytes.
XX
PS Claim 26; SEQ ID NO 16; 42pp; English.
XX
CC The invention provides novel immunoregulatory factor designated IL-X
CC which has been isolated Mycoplasma and polynucleotides encoding such
CC polypeptides. The polynucleotide is useful for augmenting proliferation
CC of B and T lymphocytes. The present sequence is Mycoplasma fermentans IL-
CC X precursor protein.
XX
XX Sequence 428 AA;

Query Match 17.0%; Score 390.5; DB 7; Length 428;
Best Local Similarity 26.8%; Pred. No. 8.4e-21;
Matches 126; Conservative 100; Mismatches 175; Indels 69; Gaps 20;

PI Webb AC, Blazar BA;
XX WPI; 2003-401108/38.
DR N-PSDB; ADK68530.
XX
XX New isolated polynucleotide, useful for augmenting proliferation of B and
PT T lymphocytes.
XX
XX Claim 12; SEQ ID NO 14; 42pp; English.
XX
XX The invention provides novel immunoregulatory factor designated IL-X
CC which has been isolated Mycoplasma and polynucleotides encoding such
CC polypeptides. The polynucleotide is useful for augmenting proliferation
CC of B and T lymphocytes. The present sequence is Mycoplasma fermentans IL-
CC X mature protein.
XX
SQ Sequence 404 AA;

Query Match 16.7%; Score 384.5; DB 7; Length 404;
Best Local Similarity 26.9%; Pred. No. 2.2e-20;
Matches 116; Conservative 89; Mismatches 155; Indels 71; Gaps 17;

QY 59 NERKEITMAKADNKH-----FGLMNAIVTAGTVNDNSFNQSWEMAI 102
DB 3 NNDSSNISFKKDKSKITTTNANGKQVKNABELKLPILITDEGKIDDSFNQSAFEBAL 62

QY 103 QQLGALTGEITSVDSSTAELEGKYSLSANTKNVWVLSGFQHGDAFTRLKIPENKOLF 162
DB 63 KAIKQKQIEINNEPES-SNFESAYNSALSAGHKIWLNGFKHQOSIKQY--IDAYREEL 119

QY 163 TEKNIILIGIDWTDENVIPTRGRYINLTYTEEAGMLAGYANASFLAKKPPSDPTKSAI 222
DB 120 ERNQIKITIGIDF-DIETEVYK--FYSLOFNKESAFITGYAIAWSLSEQ--DESKRVVA 173

QY 223 VIGGISPAYTDFIAGYLAGIKAMNLSKSDKTKI--TTDKIEINLGFVDQDTSKERLEQ 281
DB 174 SFGGGAFFGVTTFEGGAKGILYNNQKH--KSKTIHTSPVKLDSGF-----TAGCKMNT 226

QY 282 IAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVTDOSLVYTKTKNK 331
DB 227 VINNVLSSTPADVKNPHVILSVAGPAT--FETVRLANKGGYVIGVDSQGM--QDKDR 282

QY 332 FFTSILKNLGYSVFSVLSDL-----YTKKSNRNLAGFEGKKSATVYLGIDRF 381
DB 283 ILTSLVLRKIQAVETLIDLILEKEEGYKPYVVDKKDKKWSHFQTQ-----KEKW 334

QY 382 VDIADTSLGNDKKL-ATEAISEAKKEFEKTKTIIPAEVRYKTLIEIPMPD--KQPDQOE 439
DB 335 IGVAEHNFSTTEBQAKINNKIKKAIKMFKE---LPEDFVKYINSKALDKGNKIDNVSE 390

QY 440 SLDKLITDINK 450
DB 391 RLEAIIISAINK 401

RESULT 15
ADK68537
ID ADK68537 standard; procein; 404 AA.
XX
XX ADK68537;
XX
XX 06-MAY-2004 (first entry)
XX
XX Mycoplasma fermentans IL-X mature protein #2.
KM Immunoregulatory factor; IL-X; lymphocyte proliferation.
XX
XX Mycoplasma fermentans.
OS
XX US6506892-B1.
PN
XX 14-JAN-2003.
PD
XX

PF 29-OCT-1998; 98US-00182625.
XX
XX 29-OCT-1997; 97US-0063701P.
XX
XX (WEBB/) WEBB A C.
PA (BLAZ/) BLAZAR B A.
XX
XX Webb AC, Blazar BA;
XX
XX WPI; 2003-401108/38.
DR N-PSDB; ADK68535.
XX
XX New isolated polynucleotide, useful for augmenting proliferation of B and
PT T lymphocytes.
XX
XX Claim 13; SEQ ID NO 15; 42pp; English.
XX
XX The invention provides novel immunoregulatory factor designated IL-X
CC which has been isolated Mycoplasma and polynucleotides encoding such
CC polypeptides. The polynucleotide is useful for augmenting proliferation
CC of B and T lymphocytes. The present sequence is Mycoplasma fermentans IL-
CC X mature protein.
XX
SQ Sequence 404 AA;

Query Match 16.6%; Score 381.5; DB 7; Length 404;
Best Local Similarity 26.9%; Pred. No. 3.7e-20;
Matches 116; Conservative 88; Mismatches 156; Indels 71; Gaps 17;

QY 59 NERKEITMAKADNKH-----FGLMNAIVTAGTVNDNSFNQSWEMAI 102
DB 3 NNDSSNISFKKDKSKITTTNANGKQVKNABELKLPILITDEGKIDDSFNQSAFEBAL 62

QY 103 QQLGALTGEITSVDSSTAELEGKYSLSANTKNVWVLSGFQHGDAFTRLKIPENKOLF 162
DB 63 KAIKQKQIEINNEPES-SNFESAYNSALSAGHKIWLNGFKHQOSIKQY--IDAYREEL 119

QY 163 TEKNIILIGIDWTDENVIPTRGRYINLTYTEEAGMLAGYANASFLAKKPPSDPTKSAI 222
DB 120 ERNQIKITIGIDF-DIETEVYK--FYSLOFNKESAFITGYAIAWSLSEQ--DESKRVVA 173

QY 223 VIGGISPAYTDFIAGYLAGIKAMNLSKSDKTKI--TTDKIEINLGFVDQDTSKERLEQ 281
DB 174 SFGGGAFFGVTTFEGGAKGILYNNQKH--KSKTIHTSPVKLDSGF-----TAGCKMNT 226

QY 282 IAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVTDOSLVYTKTKNK 331
DB 227 VINNVLSSTPADVKNPHVILSVAGPAT--FETVRLANKGGYVIGVDSQGM--QDKDR 282

QY 332 FFTSILKNLGYSVFSVLSDL-----YTKKSNRNLAGFEGKKSATVYLGIDRF 381
DB 283 ILTSLVLRKIQAVETLIDLILEKEEGYKPYVVDKKDKKWSHFQTQ-----KEKW 334

QY 382 VDIADTSLGNDKKL-ATEAISEAKKEFEKTKTIIPAEVRYKTLIEIPMPD--KQPDQOE 439
DB 335 IGVAEHNFSTTEBQAKINNKIKKAIKMFKE---LPEDFVKYINSKALDKGNKIDNVSE 390

QY 440 SLDKLITDINK 450
DB 391 RLEAIIISAINK 401

Search completed: December 18, 2004, 01:22:19
Job time: 118.524 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2004, 01:16:03 ; Search time 30.9611 Seconds
(without alignments)
966.032 Million cell updates/sec

Title: US-09-676-249D-2

Perfect score: 2299
Sequence: 1 MKKKIKWKKELGLVLPPLS.....KPPDKQESDILITDINKN 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/p/locdata/1/1aa/5A_COMB.rep:*
- 2: /cgn2_6/p/locdata/1/1aa/5B_COMB.rep:*
- 3: /cgn2_6/p/locdata/1/1aa/6A_COMB.rep:*
- 4: /cgn2_6/p/locdata/1/1aa/6B_COMB.rep:*
- 5: /cgn2_6/p/locdata/1/1aa/PCFUS_COMB.rep:*
- 6: /cgn2_6/p/locdata/1/1aa/backfile1.rep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	393.5	17.1	428	US-09-182-625F-9	Sequence 9, Appl1
2	390.5	17.0	428	US-09-182-625F-16	Sequence 16, Appl1
3	384.5	16.7	404	US-09-182-625F-14	Sequence 14, Appl1
4	381.5	16.6	404	US-09-182-625F-15	Sequence 15, Appl1
5	225	9.8	363	US-09-583-110-2686	Sequence 2686, Ap
6	203	8.8	328	US-08-961-083-8	Sequence 8, Appl1
7	203	8.8	328	US-09-536-784-8	Sequence 8, Appl1
8	203	8.8	328	US-09-107-532A-5084	Sequence 5084, Ap
9	199.5	8.7	362	US-09-134-000C-6004	Sequence 6004, Ap
10	182	7.9	339	US-09-071-035-80	Sequence 80, Appl1
11	182	7.9	361	US-09-071-035-78	Sequence 78, Appl1
12	182	7.9	375	US-09-134-000C-6005	Sequence 6005, Ap
13	179	7.8	341	US-08-396-957A-5	Sequence 5, Appl1
14	173	7.5	166	US-09-182-625F-6	Sequence 6, Appl1
15	162	7.0	339	US-08-396-957A-4	Sequence 4, Appl1
16	149	6.5	867	US-09-540-232-2676	Sequence 2676, Ap
17	144	6.3	353	US-08-313-412-1	Sequence 1, Appl1
18	141.5	6.2	889	US-09-336-447A-15	Sequence 15, Appl1
19	141.5	6.2	889	US-09-952-267B-15	Sequence 15, Appl1
20	132	5.7	553	US-09-134-001C-2974	Sequence 2974, Ap
21	131.5	5.7	518	US-08-973-462-8	Sequence 8, Appl1
22	130.5	5.7	518	US-09-248-796A-18238	Sequence 18238, A
23	126	5.5	557	US-09-134-000C-5061	Sequence 5061, Ap
24	122.5	5.3	2285	US-09-308-375-2	Sequence 2, Appl1
25	122	5.3	2411	US-09-268-347-36	Sequence 36, Appl1
26	121.5	5.3	834	US-09-187-999-11	Sequence 11, Appl1
27	121.5	5.3	1104	US-08-923-992A-4	Sequence 4, Appl1

28	120	5.2	878	4	US-09-540-236-3401	Sequence 3401, Ap
29	119.5	5.2	1861	2	US-08-790-912-4	Sequence 4, Appl1
30	119	5.2	892	3	US-09-336-447A-5	Sequence 5, Appl1
31	119	5.2	892	4	US-09-952-267B-5	Sequence 5, Appl1
32	117.5	5.1	941	3	US-09-074-658-75	Sequence 75, Appl1
33	117.5	5.1	1073	4	US-09-206-942-49	Sequence 49, Appl1
34	117.5	5.1	1079	4	US-09-206-942-47	Sequence 47, Appl1
35	117	5.1	1912	1	US-08-409-995-4	Sequence 4, Appl1
36	117	5.1	1912	1	US-08-685-467-4	Sequence 4, Appl1
37	117	5.1	2353	3	US-09-377-155-33	Sequence 33, Appl1
38	117	5.1	2353	3	US-08-913-942-4	Sequence 4, Appl1
39	117	5.1	2353	3	US-09-669-974-33	Sequence 33, Appl1
40	117	5.1	2353	4	US-09-797-862-33	Sequence 33, Appl1
41	117	5.1	2354	4	US-09-684-707-4	Sequence 4, Appl1
42	117	5.1	2354	3	US-09-268-347-47	Sequence 47, Appl1
43	116.5	5.1	873	3	US-09-336-447A-13	Sequence 13, Appl1
44	116.5	5.1	873	3	US-09-952-267B-13	Sequence 13, Appl1
45	115.5	5.0	1164	3	US-08-923-992A-2	Sequence 2, Appl1

ALIGNMENTS

```
RESULT 1
US-09-182-625F-9
; Sequence 9, Application US/09182625F
; Patent No. 6506892
; GENERAL INFORMATION:
; APPLICANT: Webb, Andrew C.
; APPLICANT: Blazat, Beverly A.
; TITLE OF INVENTION: Polynucleotides Encoding a Mycoplasma Protein Involved in Cell Gr
; FILE REFERENCE: BLAZ-101XCI
; CURRENT APPLICATION NUMBER: US/09/182, 625F
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: US 60/063, 701
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 9
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Mycoplasma fermentans
US-09-182-625F-9

Query Match      17.1% Score 393.5; DB 4; Length 428;
Best Local Similarity 26.8%; Pred. No. 1.7e-27;
Matches 126; Conservative 101; Mismatches 174; Indels 69; Gaps 20;

QY      5 IKNNKFLGLGLVLPPLSAI-ATISAGCWDKETEKEKSDNQNKQITDVSKISGLVNERKS 63
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MKSKSKITLGL-SPIALILPAVANVSCGNDES-----NISFKKDISKVTTNANGKO 52

QY      64 EIMAAKDANKHGLNMAIYTAGTVNDSFNQSSWALIQGLALTGCEITSVDNSTAEL 123
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      53 VVKNAEL-----LTKLKITLITDEGKIDKSFNQSAPFALAINKQGTIEINNVPS-SNF 106

QY      124 EGKSSSLANTNNKVVVSGFOHGAFTRWLKIPIENKQLFTFKNLIIIGIDTDENVLP 183
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      107 ESNATSLSSGKHKIWLNVGFRHQOSIKQY-IDAHRELEBNQIKITIGIDE-DLETXYK 163

QY      184 GRYINTLYKTEAGWLAGVANASFLAKKPPSDPTKRSAYIYGGISPAVDFIAGYLAGI 243
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      164 --FVSLQFNKESAFITGVAIASWLSQ---DESKRVASFGGAPGVTFNNGFAKGI 218

QY      244 KAMTLKSDKTKI-TTDKLEINIGFVQDSTYERLEQIAS-----KDKESTLL 292
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      219 LLYNQKH--KSKSKYHTSPVKLDSGF-----TAGKKNVTYINNVLSSTPADVKYNPVIL 271

QY      293 AVAGPLLEIFSDIANDRYLIGVDPDQSLVYTKTKNFFSTILKXIGYSVFLSDL- 351
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      272 SVAGPAT--FETVYLANKGQVIGVSDQGM--QDKDRILTSVLKIKQAVETFLDLI 327

QY      352 -----YTKKSNHNLGAFEPGKSKATVYIGIKDRFVDIADTSLGNDKGL-ATEAI 401
```

```
Db      328 LEKEEGKPPYVVKKKADKKMSHFQTQ-----KEMWIGVANNHNSNTSEOKAKINKKI 379
Qy      402 SEAKKEFEKTKTTPAEVRKLTLEIPEMPD-KQPDKQOESLDTITDINK 450
      380 KEAIKMKPE-----LPEDFVKYKINSDDKALKDGNKIDNVSERLEAIIISAINK 425

RESULT 2
US-09-182-625F-16
; Sequence 16, Application US/09182625F
; Patent No. 6506892
; GENERAL INFORMATION:
; APPLICANT: Webb, Andrew C.
; APPLICANT: Blazar, Beverly A.
; TITLE OF INVENTION: Polynucleotides Encoding a Mycoplasma Protein Involved in Cell Gr
; FILE REFERENCE: BLAZ-101XC1
; CURRENT APPLICATION NUMBER: US/09/182,625F
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: US 60/063,701
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 16
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Mycoplasma fermentans
US-09-182-625F-16

Query Match      17.0%; Score 390.5; DB 4; Length 428;
Best Local Similarity 26.8%; Pred. No. 3.3e-27;
Matches 126; Conservative 100; Mismatches 175; Indels 69; Gaps 20;

Qy      5 IKMKKPLGLGLVPLPSAI-ATISAGCWDKETTKEKSDNQNKOITDVSKISGLVNERKS 63
      1 MKSKKTLILGL-SPILAILPAVAVSCGNDES-----NISFKKOISKYTTTNANGKQ 52
Db      64 EIMAAKADANKHFGLNMAIYTAGTVNDNSFNQSSWEAIQOLGALTGEETSVDSIAEL 123
      53 VVKNAEL-----LKLKPLILITDEGKIDKSFNQSFAFEALKAINKQTGIEINNVEPS-SNF 106
Qy      124 EGKSSSLANTNKNVWVLSGFQHGDAFTRMKLIPEMKOLFTEKNIIILIGIDWTDENVIPT 183
      107 ESNYNSALSAGHKIWLNGFPGQOSIKOY--IDAHELELNQIKITIGIDF-DIETEKW 163
Qy      184 GRYINLYKTEEAGMLAGYANASFLAKKFPSPDKSAIYIGGGISPAVTDPIAGYLAGI 243
      164 --FYSLOFNIKESAFITGYAIAWSLSEQ--DESKRVVASFGGAFPGVTTFNNGFAKGI 218
Qy      244 KANWLKNSDKTKI--TTDKIEINLGFVDVQDTSTYERLEQIAS-----KDKPSTLL 292
      219 LYVNOQKH--KSSKIYHTSPVLDISGF-----TAGEKMAVTVINNVLSSTPADVKYNPHVIL 271
Qy      293 AVAGPLEIFSDIIANQNDRLIGVDTPDOSLVYTKTKNKFSTSLIKNLGVSFVLSL 351
      272 SVAGPAT--FETVYLANKGQYVIGVDSQGM--QDKRIITFVLAHKIKQAVYETLLDLI 327
Qy      352 -----YTKSNSRNLAGFEFGKSAFTVYLGIKDFVYDIADTSLGNDKKU-ATEAI 401
      328 LEKEEGKPPYVVKKKADKKMSHFQTQ-----KEMWIGVANNHNSNTSEOKAKINKKI 379
Qy      402 SEAKKEFEKTKTTPAEVRKLTLEIPEMPD-KQPDKQOESLDTITDINK 450
      380 KEAIKMKPE-----LPEDFVKYKINSDDKALKDGNKIDNVSERLEAIIISAINK 425

RESULT 3
US-09-182-625F-14
; Sequence 14, Application US/09182625F
; Patent No. 6506892
; GENERAL INFORMATION:
; APPLICANT: Webb, Andrew C.
; APPLICANT: Blazar, Beverly A.
```

```
; TITLE OF INVENTION: Polynucleotides Encoding a Mycoplasma Protein Involved in Cell Gr
; FILE REFERENCE: BLAZ-101XC1
; CURRENT APPLICATION NUMBER: US/09/182,625F
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: US 60/063,701
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 14
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mycoplasma fermentans
US-09-182-625F-14

Query Match      16.7%; Score 384.5; DB 4; Length 404;
Best Local Similarity 26.9%; Pred. No. 1.1e-26;
Matches 116; Conservative 89; Mismatches 155; Indels 71; Gaps 17;

Qy      59 NERKSEIMAAKADANKI-----FGLNMAIYTAGTVNDNSFNQSSWEAI 102
      3 NNEBSNISFKKIDSKYTTTNANGKQVKNABELKLPILITDEGKIDKSFNQSFAFEAL 62
Qy      103 QOLGALTGEETSVDSIAELGKYSLSANTNKNVWVLSGFQHGDAFTRMKLIPEMKOLF 162
      63 KAIKQOTGIEINNVEPS-SNFESEAYNSALSAGHKIWLNGFPGQOSIKOY--IDAHELE 119
Qy      163 TEKNIIILIGIDWTDENVIPTGRYINLYKTEEAGMLAGYANASFLAKKFPSPDKSAI 222
      120 ERNQIKITIGIDF-DIETEKW--FYSLOFNIKESAFITGYAIAWSLSEQ--DESKRVVA 173
Qy      223 VIGGISPATYTDPIAGIAGIKANLKNSSDKTKI--TTDKIEINLGFVDVQDTSTYERLEQ 281
      174 SFGGAFPGVYTFNNGFAKGI LYVNOQH--KSSKIYHTSPVLDISGF-----TAGEKMAVT 226
Qy      282 IAS-----KDKPSTLLAVAGPLEIFSDIIANQNDRLIGVDTPDOSLVYTKTKN 331
      227 VINNVLSSTPADVKYNPHVILSVAGPAT--FETVYLANKGQYVIGVDSQGM--QDKR 282
Db      332 FPTSILKNLGVSVFVLSLSDI-----YTKSNSRNLAGFEFGKSAFTVYLGIKDF 381
      283 ILTSLKHIKQAVYETLLDLILEKEEGKPPYVVKKKADKKMSHFQTQ-----KEKW 334
Qy      382 VDIADTSLGNDKKU-ATEAISEAKKEFEKTKTTPAEVRKLTLEIPEMPD-KQPDKQOE 439
      335 IGALENHFSNTEBQAKINKKI KEAIKMKPE-----LPEDFVKYKINSDDKALKDGNKIDNVSE 390
Qy      440 SLDKLITDINK 450
      391 RLEAIIISAINK 401
Db

RESULT 4
US-09-182-625F-15
; Sequence 15, Application US/09182625F
; Patent No. 6506892
; GENERAL INFORMATION:
; APPLICANT: Webb, Andrew C.
; APPLICANT: Blazar, Beverly A.
; TITLE OF INVENTION: Polynucleotides Encoding a Mycoplasma Protein Involved in Cell Gr
; FILE REFERENCE: BLAZ-101XC1
; CURRENT APPLICATION NUMBER: US/09/182,625F
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: US 60/063,701
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 15
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mycoplasma fermentans
US-09-182-625F-15

Query Match      16.6%; Score 381.5; DB 4; Length 404;
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Best Local Similarity 26.9%; Pred. No. 2e-26;
Matches 116; Conservative 88; Mismatches 156; Indels 71; Gaps 17;

QY 59 NERSEITMAKADANKH-----FGLMAIYTAGTNDNSFNSSWEAI 102
DB 3 NNESENISFEKEDISKYTTTNANGKOVVKAELLKPIILITDGBKIDDKSFNOSAREAL 62
QY 103 QOQALGGEITSDSSFALEGGYSSILANTNKVWVLSGFQHDADFRLMKIPENKOLF 162
DB 63 KAIKQJGIEINNVPS-SNESAYNALSNGHKIYWLNGFKHOOSIKQY--IDAYEBEL 119
QY 163 TEKNIILIGIDWTDENVIPTRGRYINLYKTEAGWLAGVANASFLAKKPPSDPTKSAI 222
DB 120 ERNODIKIIGIDF-DIETEVKW--FYSIQFNIKESAFITGVAIASWLSQ--DESKRVVA 173
QY 223 VIGGIGIPATYDFLAGLAGIKAMNLSKDKTKI--TTDKIEINLGPVODTSTKERLEQ 281
DB 174 SFGGGAFFGVTTFEGGPAKGLIYVNOQH--KSSKIYHTSPVKLDSGF----TAGEKMT 226
QY 282 IAS-----KDPSTLLAVAGPLTEIFSDIIANONDRYLIGVDTQSLVYTKTKNK 331
DB 227 VINNVLSSTADVKNHVLISVAGPAT--FETVRLANKQGYVIGVSDQGM--QDKDR 282
QY 332 FETSILKNLGYSPSVLSDL-----YTKKSNRNLAGFEGKKSATVYLGIKDRF 381
DB 283 ILTSVLKHIQAVYETLLDLILEKEGKYPVVDKADKKMSHFQV-----KEXW 334
QY 382 VDIADTISLEGNDKL-ATEAISEAKKEFEETKTIIPAEVRAKTEIEMPD-KOPDKOE 439
DB 335 IGAENHFSNTEBQAKINNKIKAIKMFKE---LPEDFVYKINSKALKDKGNKIDNVSE 390
QY 440 SLDKLTIDNK 450
DB 391 RLEAIIAISINK 401

RESULT 5

US-09-583-110-2686
Sequence 2686, Application US/09583110
Patent No. 6699703
GENERAL INFORMATION:
APPLICANT: Lynn Docette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
FILE REFERENCE: PAT400-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 2686
LENGTH: 363
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-583-110-2686

Query Match 9.8%; Score 225; DB 4; Length 363;
Best Local Similarity 24.8%; Pred. No. 3.9e-12;
Matches 110; Conservative 61; Mismatches 150; Indels 122; Gaps 21;

QY 1 MKKKIKNNKFLGLVPLSLAIAITIS-AGCWDKETTEEKADNONKOITVSKISGLVN 59
DB 14 MNKK-----QWLGGLV-----AVALVGLAACNRSSRNAASSSDVYTK-----52
QY 60 ERKEIIMAAKADANKHGLNMAIYTAGTVNDNSFNSSWEAIQOLG---LTGGETITSV 116
DB 53 -----AAIVTDGVDKDSFNOSAMWGLQAWGKEHNLKDNKGFTY 92
QY 117 DSGTALE-----GKYSILANTNKVWVLSGFQHDADFRLMKIPENKOLFTEKNI 167

DB 93 FOSTSEADYANNLQQAAGSYNLI-----FGVGFALHNAVEBAKHTDLNY 138
QY 168 IILIGIDWTDENVIPTRGRYINLYKTEAGWLAGVANASFLAKKPPSDPTKSAIIVGCG 227
DB 139 VLIDVIVKDKV-----ASVTFADNESGYLAGVAAK-----TTTKOVGVGG 183

QY 228 I-SPAVDFLAGYLAGIKAMNLSKDKTKITTDKIEINLGFVODTSTKERLEQIASKD 286
DB 184 IESVIRFPAFGPAV-----ASVDSIVQVDYAG-SFG-DAAKGTIAAQAAGAD 236
QY 287 KPSTLLAVAGPL-TEIFSDIIANONDR-----YLIGVDTQSL-VYT-----TKQKFF 333
DB 237 ---IVYQVAGTGAGVAFKAASLINESRPERNEKVVIVIDRDOEAGKYSKDGKESFVL 293
QY 334 TSILKNLGYSPSVLSLTYTKKSNRLAGFERGKSATYVLGIKDRFVDIADTISLEND 393
DB 294 VSTIKQVGTIVKDI-----SNKAEKGFPGSQ--VIVYSKDGVDLAVNLSEBG 342
QY 394 KKLATEAISEAKKEFEETKTIIP 416
DB 343 KK-----AVEDAKAKIIDGSVKVP 361

RESULT 6

US-08-961-083-8
Sequence 8, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-083-8

Query Match 8.8%; Score 203; DB 3; Length 328;
Best Local Similarity 25.7%; Pred. No. 3.4e-10;
Matches 98; Conservative 56; Mismatches 144; Indels 84; Gaps 19;

QY 61 RKSEIIMAAKADANKHGLNMAIYTAGTVNDNSFNSSWEAIQOLG---LTGGETITSVD 117

Db 3 RSSRNASSSDVK---TKAAIVTDGTGVDKSFNQASMEGLQMGKEHNLKONGFTYF 58
Qy 118 SSTAEL-----GKYSILANTKNKWNVLGFGHGDFAFTRMLKIPENKOLFTEKNII 168
Db 59 QSTSEADYANNLQQAAGSYNLI PGV-----GALNNA-----VKDAKHEHTDLNIV 104
Qy 169 ILIGIDWTDENVITPTGRYINLTYTEAGMLAGYANASFLAKKPPSDPTKSAIVIGGI 228
Db 105 LIDVIVDQKNV-----ASVTFADNBSGYLAGVAAAK-----TTKTKQVFPVGGI 149
Qy 229 -SPAVIDPIAGYLAGIKAMNLKNSDKTKITTDKIEINLGFVDPTSTKERLEQIASDK 287
Db 150 ESEVISFEAGFKAGV-----ASVDPSIKQVDYAG-SFG-DAKAKGTIAAQYAAAGAD- 201
Qy 288 PSTLLAVAGPL-TEIFSDIANQDR-----YLIGVDTQSL--VYT---KTKNKEFT 334
Db 202 --IYQVAGGTGAGVFAEAKSLNESRPNENKRWYIGVDRQDEAGKYSKDGKSNFVLV 259
Qy 335 SILKNLGYSVPSVLDLYTKKNSRNLAGEFEGKKSATVYIGIDRFVDIADTSLSENDK 394
Db 260 STLKQVGTIVKDI-----SNKAERGEFPGGQ--VIYVSLKDKGVDLAVTNLSEBGK 308
Qy 395 KLATEAISEAKKEFEKTKTIP 416
Db 309 K---AVEDAKAKILDGSKVP 326

RESULT 7

US-09-536-784-8
Sequence 8, Application US/09536784
Patent No. 6573082

GENERAL INFORMATION:

APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/536,784

FILING DATE: 30-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/961,083

FILING DATE: OCT-30-1997

ATTORNEY/AGENT INFORMATION:

NAME: Michelle S. Marks

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB340P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 328 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-536-784-8
Query Match 8.8% Score 203, DB 4, Length 328,
Best Local Similarity 25.7% Pred. No. 3.4e-10;

Matches 98; Conservative 56; Mismatches 144; Indels 84; Gaps 19;
Qy 61 RKSEIMAAKADANKHFGIANNAYTAGTYVNDNSFNQSWEAIQOLA---LTGGEITSVD 117
Db 3 RSSRNASSSDVK---TKAAIVTDGTGVDKSFNQASMEGLQMGKEHNLKONGFTYF 58
Qy 118 SSTAEL-----GKYSILANTKNKWNVLGFGHGDFAFTRMLKIPENKOLFTEKNII 168
Db 59 QSTSEADYANNLQQAAGSYNLI PGV-----GALNNA-----VKDAKHEHTDLNIV 104
Qy 169 ILIGIDWTDENVITPTGRYINLTYTEAGMLAGYANASFLAKKPPSDPTKSAIVIGGI 228
Db 105 LIDVIVDQKNV-----ASVTFADNBSGYLAGVAAAK-----TTKTKQVFPVGGI 149
Qy 229 -SPAVIDPIAGYLAGIKAMNLKNSDKTKITTDKIEINLGFVDPTSTKERLEQIASDK 287
Db 150 ESEVISFEAGFKAGV-----ASVDPSIKQVDYAG-SFG-DAKAKGTIAAQYAAAGAD- 201
Qy 288 PSTLLAVAGPL-TEIFSDIANQDR-----YLIGVDTQSL--VYT---KTKNKEFT 334
Db 202 --IYQVAGGTGAGVFAEAKSLNESRPNENKRWYIGVDRQDEAGKYSKDGKSNFVLV 259
Qy 335 SILKNLGYSVPSVLDLYTKKNSRNLAGEFEGKKSATVYIGIDRFVDIADTSLSENDK 394
Db 260 STLKQVGTIVKDI-----SNKAERGEFPGGQ--VIYVSLKDKGVDLAVTNLSEBGK 308
Qy 395 KLATEAISEAKKEFEKTKTIP 416
Db 309 K---AVEDAKAKILDGSKVP 326

RESULT 8

US-09-107-532A-5084
Sequence 5084, Application US/09107532A
Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Walcham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 5084:

SEQUENCE CHARACTERISTICS:

LENGTH: 374 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHEICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: mlec.feature
LOCATION: (B) LOCATION 1...374
SEQUENCE DESCRIPTION: SEQ ID NO: 5084
US-09-107-532A-5084

Query Match 8.8%; Score 203; DB 4; Length 374;
Best Local Similarity 25.2%; Pred. No. 4.3e-10;
Matches 95; Conservative 64; Mismatches 132; Indels 86; Gaps 19;

QY 81 AIVTAGTVNDNSFNQSSWEAIIQOLGALTGEITSVSTALEGKTSYSLANTKNVWV-139
DB 58 ALITDTGVDNRSTNQSAMELEKMKK-----DQGLSRKNDGPOYRQSSNESDYIP-108
QY 140 -----LSGFQ--HGDAFTRWLKI PENKQLETKNIILG--IDWTDENVIPTRYINTL-189
DB 109 NIDQALNAGFKTIPGIGYKLPALIOEQATNNTGTNFVIDDVLGLD--NV-----VSA-160
QY 190 TYTTEEGMVLGYNASFLAKKFPSPDPTKSAIYIGGISPAVVD--PIAGVLAKIKAMNL-248
DB 161 TPKDNESAYLAGVAAV-----TLETNVVGFIGVGKEVIDRFDAGFKAGVDA-GA-210
QY 249 KNSDKTKRITTDKLEINLGFVDOTSTERLEQIA---SKDKPSTLLAVAGPLTEIFSD-304
DB 211 KELGKEIKV-----LNVYAGDFSPAPDKRSIAQCMYAKNADIIIFHASSGTGNGVFOE-262
QY 305 I--IANONDR--YLIGVDTDS-----LVYTKTKNKEFTSLIKNLGYSVPSVLSDLTYTK-355
DB 263 AKSLNESGDKKVMYIGVDRDQSDGEYTLNGEKKNFTLSTLKAVG---TVVEDLAKS-318
QY 356 SNRNLGAFERKGSATVYLGIKRFPDIADTSLGNDKXKATATSAIKAEFEKRTKI-415
DB 319 ADGK-----PFGGEHTVY--GLKEDGVGLTEGQLSDAKK---AVDEAKKI-----360
QY 416 PAEEVRKLTLEIPEMPDK-432
DB 361 -----ISGDVAVPEETPEE-373

RESULT 9
US-09-134-000C-6004
Sequence 6004, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patent version 3.1
SEQ ID NO 6004
LENGTH: 362
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-6004

Query Match 8.7%; Score 199.5; DB 4; Length 362;
Best Local Similarity 23.3%; Pred. No. 8.5e-10;
Matches 107; Conservative 69; Mismatches 152; Indels 131; Gaps 20;
QY 3 KIKMKNFLGIGLVPISATITISAGCWDKTTKEBSADNQNQITDVSKITISGLVNERK-62
DB 4 RKVQAQFLGIGLAAVALLTIGLAACGNSKKNANTKQDPQHSVVMVTD-----51
QY 63 SEIMAAKADANKHGLNMAIVTAGTVNDNSFNQSSWEAIIQOLGALTGEITSVDSSTAE-122

DB 52 -----TAG--IDDKSFNQSANEQEWG--KEHKLPEGPQGVAV-86
QY 123 LEGKYSSTANTKNKVMVLSGFQ--HGDAFTRWLKI PENKQLETKNIILGIDWTDENV-180
DB 87 IQSNEADYTSNIDQAISSQFKTIFGIGYLLKNAVDAADNPETNVLV----DPTVN-141
QY 181 IPTGRYINLTYKTEEAGMVLGYNASFLAKKFPSPDPTKSAI--VIGGISPAVTDPIAGY-239
DB 142 -GRNNVASATFRDNESAYLAGVAAA-----NTTKNVVGFIGVEGPIGRFOAGF-191
QY 240 LAGIKAMNLKNSDKTKITTDKLEINLGFVDOTSTERLEQIASKQKPSLLAVAGPLT-299
DB 192 EKV-----ADAGK-----LGKDIQITSTYAGTFADASKGR-----ALASSMY-230
QY 300 EIFSDII-----ANONBRYLIGVDTDSL--VT-----KTRNKF-332
DB 231 QAGADITTHAAATTGGQIFQBAKALNTGSKDKKVMYIGVDRDQSDGKTTKQKDNLT-290
QY 333 FTSILKNLGYSVPSVLSDLTYTKSNSHNLGAFERKGSATVYLGIKRFPDIADTSLGNN-392
DB 291 LAGTIKGVNIIV--KKISDLALEDK-----PFGGEH--LTVGLKQDGYD-----330
QY 393 DKLATETALG--EAKFEFEKTKTIPAEVRKLTLEIPEMP-430
DB 331 -----LTTEALSDQATVAKAEKQIISGDV-----VPDOP-362

RESULT 10
US-09-071-035-80
Sequence 80, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-80

Query Match 7.9%; Score 182; DB 4; Length 339;
Best Local Similarity 25.4%; Pred. No. 3.1e-08;
Matches 104; Conservative 51; Mismatches 139; Indels 116; Gaps 20;

```

QY      61 EKSEIEMAKDANKHFGJLMAIVTGAQTJNDSPNOSMEALIOQLA-----LTCGB----- 112
Db      7 KTAEBGGGKGDA---AHSAVIITDTGGVDDSPNOSMEGLAMCKEHDLPBGSGCYAY 62
QY      113 ITSVDS--TALBEGKYSILANTNRKNWVLSGFQHDGDAFTRMWKIPENKOLFTEKNIIL 170
Db      63 IQSNDAADYTTNIIDQAVSKFNTIFQI-----GYLLKDA-----ISSADANPDNTFVLI 112
QY      171 GIDWTDTENVLPTRKYNILTYKTEBAGMLAGYANMSFLAKKPPSDPTKSAIYIGGSI 230
Db      113 DDQIDGKKNV-----VSATFRDNEAAYIAGYAAA-----NETKTNKGFVGGEBS 157
QY      231 AVTD-FIAGYLAGIKAMMLKNSDKTKITTDKIEINLGFVDQDTSRKERLEQJASDKDS 289
Db      158 VVIDRFQGFGEFV-ADAAKEIGKEITVDT-----KTAASPADPA 196
QY      290 TLLAVAGFLTEIFSDII-----ANQNR-YLIGVDTQSL--VYT 326
Db      197 KGKMLAAMYNQGVIIIFASGATQGVQFEAKDNESGSGDKWVIGVDRDDADAGKY- 255
QY      327 KTK-----NKEFTSILKNGISVFSVSLDYTKKSNRNLAGFEFGKSGATVYLGIKDRF 381
Db      256 KTKQGEKDNFTLTSLKGVTGAVODIANRLEDK-----PFGGHLVY-GKDDG 304
QY      382 VDIADTSLGNDKCLATEAISEAKKEFEKTKTPIAEVRKTLTEIPEMD 431
Db      305 VDLTDGYI--NDKT-----KAAYTAKDKVIGSDGVKEBEKE 339

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```

RESULT 11
US-09-071-035-78
: Sequence 78, Application US/09071035
: Patent No. 6448043
: GENERAL INFORMATION:
: APPLICANT: Gil H. Choi
: TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
: NUMBER OF SEQUENCES: 496
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
: COMPUTER: HP Vectra 486/33
: OPERATING SYSTEM: MSDOS version 6.2
: SOFTWARE: ASCII text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/071,035
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: A. Anders Brookes
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PB369P2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 78:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 361 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: JS-09-071-035-78

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	Query Match	7.9%;	Score 182;	DB 4;	length 361;	
	Best Local Similarity	25.4%;	Pred. 0.3,4e-08;			
	Matches	104;	Conservative	51;	Mismatches 139;	Indels 116; Gaps 20;
QY	61	RKSSIMAAKADANKHFGELNMAIVTAGGTVDNDSFNQSWSEAIQQLGA--LTGE-----	112			
DB	29	KTASGGGKGDA-----ASHAVIITDTGVDGDDKSFNOSWSEGLQWKGKHDPREGSKGAY	84			
QY	113	ITSDSS--TALBEGKSSLANTNKNWVLSFGQHGAFWTMLKIPENKQLFTEGNIIIL	170			
DB	85	IQSDNADAYTNIDQAVSSKFNITFGI---GYLLKDA-----ISSAADNPDTNFVLI	134			
QY	171	GIDWTDTEENVIPTRGRYINLTGYTEAGWLAGYANASFLAKKFPSDPTKRSATVIGGGISP	230			
DB	135	DDQIDGKKNV-----VSATFRDNEAIVLAGVAAA-----NETKTNKGVFGVBEG	179			
QY	231	AVTD-FLAGYIAGIKAMNKNKSDKTKITTDPKIEINLGFVDYDQISTKRLLEQIASKDKPS	289			
DB	180	VVIRFQGFPEKGV-ADAANKELGKEITVDT-----RYAASFADPA	218			
QY	290	TLAVAGLTERIPSDII-----ANQDR-VLIGVPTDQSL--VYT	326			
DB	219	KGKALLAAMYNGVDIIIFHSGATGCGVFGFAKDLNBSGSDKRWVIGVDNDQADAGKX	277			
QY	327	KTK-----NKEFTSILKNLGYSVFSVLSDLTYTKKSNSBNLAGFEFGKKSATVYIGIDRF	381			
DB	278	KTKGKEDNFLTITLKGVGTAVODIANRALEDK-----FPQGEHLVY-GLXDG	326			
QY	382	VDIADTSLGNDKLLATEAISAKKEPEPEKTKTIPAEVTKLTLEPEMD	431			
DB	327	VDLTGCVL--NDKT-----KEAVKIAKDKVISCVDVAVPEKPE	361			

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RESULT 12
US-09-134-000C-6005
; Sequence 6005, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134, 000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6005
; LENGTH: 375
; TYPE: PRF
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6005

Query Match          7.9%; Score 182; DB 4; Length 375;
Best Local Similarity 25.4%; Pred. No. 3.6e-08;
Matches 104; Conservative 51; Mismatches 139; Indels 116; Gaps 20.

QY      61  RKSEIMAKADANGHFGILNMAIVTAGGTVDNNSFNOSWEAIIQOLGA---LTGGE----- 112
DB      43  KTAASGGGKGGA-----AHSAAVITIDTGGVDDKSFNOSWEGLOAMGKEHDLPEGSKGYAY  98
QY      113 ITSVDS--TALBEGKYSLSANTNKNWVLSGFQHGAFTRWLKI PENKOLFTEKNIIIL 170
DB      99  IQSDADADYTTINQAVNSSKNTIFGI-----GYLLKDA-----ISSAADANPDTNFVLI 148
QY      171 GIDWTDTEWVIFPTGRYINLTYKTEBAGMLAGYANASFLAKFPBDDPTKRSATVIGGGISP 230
DB      149 DDQIDGKKGV-----VSATFRDNEAAVLAGVAAA-----NETYTNKVGFEVGGREG 193
QY      231 AVTD-PLAGYIAGIKANMLKNSDKKTIITDPIKIEINLGFVDYDTSTKERLEQIASKDPS 289
DB      194 VVIRFQAGFEKGV-ADAAKEIGETIVDT-----RYAASFADPA 232

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QY 284 S-----|K|P|E|T|L|A|V|A|G|P|L|E|P|S|D|I|A|N|Q|N|R|Y|I|G|V|T|O|O|S|L|Y|T|K|K|F 333
Db 55 N|N|V|L|S|T|P|A|D|V|K|N|P|H|V|I|L|S|V|A|G|P|A|T|---P|E|Y|R|A|N|K|Q|Y|I|G|V|D|S|D|G|M|---Q|D|K|R|L 110
QY 334 T|S|I|L|K|N|G|Y|S|V|E|S|V|S|D|L|-----Y|T|K|S|N|R|N|A|G|E|F|G|K|S|A|T|Y|V|L|G|I|K|D|F|V|D 383
Db 111 T|S|V|L|K|I|K|A|V|A|V|E|T|L|D|L|I|L|E|K|E|G|Y|K|P|Y|V|V|D|K|K|A|D|K|K|W|H|F|G|T|O|-----K|E|K|W|I|G 162
QY 384 I|A|D 386
Db 163 V|A|E 165

RESULT 15
US-08-396-957A-4
Sequence 4, Application US/08396957A
Patent No. 5780041
GENERAL INFORMATION:
APPLICANT: SIMPSON, WARREN; SCHMAN, TOM G.
TITLE OF INVENTION: ANTIGENIC PROTEINS AND
TITLE OF INVENTION: GENES ENCODING SAME OF BORRELIA BURGDORFERI.
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,957A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/020,245
FILING DATE: 19-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/664,731
FILING DATE: 05-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,716
FILING DATE: 05-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2066-4018USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 339
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Borrelia burgdorferi
STRAIN: Sh-2-82
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:

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: ORGANELLE:
: FEATURE:
: ?
: ? NAME/KEY: p39'
: ? LOCATION:
: ? IDENTIFICATION METHOD:
: ? OTHER INFORMATION: p39', protein
: ? OTHER INFORMATION: sequence.
US-08-396-957A-4

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Query Match	7.0%;	Score 162;	DB 1;	Length 339;
Best Local Similarity	22.8%;	Pred. No. 2.1e-06;		
Matches	85;	Conservative	69;	Mismatches 135;
			Indels	84;
			Gaps	18;

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QY      87 GTVNDNSPFOSSWEBAIQOLGALTGGEIITSVDSST-----AELEGKYSLSANTNRVWLISG 142
Db      37 GTFDSDSFPNESHNLNVQVKYKBEFKIELVAKSSSSNSVSLDLEG-----LKGAGSLLIWLIG 92

QY      143 FOHGD-AFTRWLKITPENKQLFTEKNIIILIGIDWTDTENVIPTRGYINULYKTEBACHLAG 201
Db      93 YRFSVDYAKAAALQNDPMKXAI-----IDPIYSNDPIP-ANLVMTERRAEGAFILTG 142

QY      202 YNASTIACKFPSPDPTKSAIYIGGSIAPATD-FINGYLAGIYAWMLKNSDKKTKITTD 260
Db      143 YIAAKL-----SKTGKIGFGLGEGEIVDAFRGYEGAGAYXAN-----KDIKISTQ 188

QY      261 KI-----EINLGFVDQDSTFKERLEQIASKDKPSTLLAVAGLPIEFSDIIANQ--NDRYL 314
Db      189 YISFADLDEAGSVAATRYMSDEID-----IIHHAAGLGIGALIVAKELGSGHYI 238

QY      315 IGVDTDQSLVYTKTKNKKFTSILKNLGYSVFSVSLDLYTKKSNRNLAGEFGKGSATVY 374
Db      239 IGVDEDDQAVL--APDNVITSTTKQVGRAL-----NIFT--SNHLKTNTFEGGK--LIN 285

QY      375 LGIKDRFVDIADTSLSGNDKDLATATAIABAKKEFEKTKITIIPAEVAVKTEIEPMPKOP 434
Db      286 YGLKEGVAVFV-----RNPKNISF-----ELEKEIDMLSKIKKEIIVP----- 325

QY      435 DKQOESGLDKLITD 447
Db      326 -SNKESYEKFLXK 337

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Search completed: December 18, 2004, 01:28:35
Job time : 33.9611 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2004, 01:26:40 ; Search time 104.236 Seconds
(without alignments)
1548.256 Million cell updates/sec

Title: US-09-676-249D-2
Perfect score: 2299
Sequence: 1 MKKKIKMKFLGLVPLS.....KPPDKQESLDTITINKN 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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13: /cgnt_6/ptodaca/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgnt_6/ptodaca/2/pubpaa/US10_PUBCOMB.pep:*
15: /cgnt_6/ptodaca/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgnt_6/ptodaca/2/pubpaa/US10C_PUBCOMB.pep:*
17: /cgnt_6/ptodaca/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgnt_6/ptodaca/2/pubpaa/US11_NEW_PUB.pep:*
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20: /cgnt_6/ptodaca/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	232.5	10.1	350	US-10-474-792-166	Sequence 166, App
2	223	9.7	350	US-09-769-337-132	Sequence 132, App
3	221	9.6	344	US-10-451-337-6	Sequence 6, Appl
4	217.5	9.5	330	US-10-451-337-12	Sequence 12, Appl
5	217.5	9.5	330	US-10-451-337-14	Sequence 14, Appl
6	217.5	9.5	330	US-10-451-337-39	Sequence 39, Appl
7	217.5	9.5	330	US-10-451-337-40	Sequence 40, Appl
8	214.5	9.3	330	US-10-451-337-16	Sequence 16, Appl
9	214.5	9.3	330	US-10-451-337-42	Sequence 42, Appl
10	214.5	9.3	328	US-09-765-272-8	Sequence 8, Appl
11	188.5	8.2	347	US-10-451-337-8	Sequence 8, Appl
12	188.5	8.2	347	US-10-451-337-8	Sequence 8, Appl
13	188.5	8.2	347	US-10-474-792-180	Sequence 180, App

14	182	7.9	339	US-09-071-035-80	Sequence 80, Appl
15	182	7.9	339	US-10-206-576-80	Sequence 80, Appl
16	182	7.9	361	US-09-071-035-78	Sequence 78, Appl
17	182	7.9	361	US-10-206-576-78	Sequence 78, Appl
18	173	7.5	166	US-09-760-541-6	Sequence 6, Appl
19	169	7.4	357	US-10-282-122A-60484	Sequence 60484, A
20	156	6.8	797	US-10-156-761-10907	Sequence 10907, A
21	150	6.5	223	US-09-769-736-48	Sequence 48, Appl
22	141.5	6.2	889	US-09-952-267-15	Sequence 15, Appl
23	131.5	5.7	1786	US-09-742-096-3	Sequence 3, Appl
24	131.5	5.7	1787	US-10-415-253-2	Sequence 2, Appl
25	130.5	5.7	496	US-10-451-467A-432	Sequence 432, App
26	123.5	5.4	998	US-10-282-122A-70450	Sequence 70450, A
27	123.5	5.4	1031	US-10-282-122A-54611	Sequence 54611, A
28	122.5	5.3	2045	US-10-282-122A-74463	Sequence 74463, A
29	122.5	5.3	2059	US-10-474-792-62	Sequence 62, Appl
30	122.5	5.3	2285	US-09-932-183A-2	Sequence 2, Appl
31	121.5	5.3	852	US-10-282-122A-62892	Sequence 62892, A
32	121.5	5.3	1104	US-09-797-385-4	Sequence 4, Appl
33	120.5	5.2	2457	US-10-282-122A-49854	Sequence 49854, A
34	120	5.2	719	US-10-239-610-2	Sequence 2, Appl
35	119	5.2	776	US-10-238-075-571	Sequence 571, App
36	119	5.2	892	US-09-952-267-5	Sequence 5, Appl
37	119	5.2	902	US-10-437-963-105564	Sequence 105564, A
38	118.5	5.2	1963	US-10-282-122A-73978	Sequence 73978, A
39	118.5	5.2	2872	US-10-282-122A-60137	Sequence 60137, A
40	118	5.1	571	US-10-282-122A-70208	Sequence 70208, A
41	118	5.1	896	US-10-282-122A-60816	Sequence 60816, A
42	118	5.1	1849	US-10-637-544-2	Sequence 2, Appl
43	117.5	5.1	1073	US-10-193-764-45	Sequence 45, Appl
44	117.5	5.1	1079	US-10-193-764-43	Sequence 43, Appl
45	117.5	5.1	6641	US-10-282-122A-70580	Sequence 70580, A

ALIGNMENTS

```
US-10-474-792-166
: Sequence 166, Application US/10474792
: Publication No. US20040236072A1
: GENERAL INFORMATION:
: APPLICANT: Olmsted, Stephen
: APPLICANT: Zagursky, Robert
: APPLICANT: Nickbarg, Elliot
: APPLICANT: Winter, Laurie
: TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
: FILE REFERENCE: AM 100399
: CURRENT APPLICATION NUMBER: US/10/474,792
: CURRENT FILING DATE: 2003-10-14
: NUMBER OF SEQ ID NOS: 674
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 166
: LENGTH: 350
: TYPE: PRT
: ORGANISM: Streptococcus pyogenes
US-10-474-792-166
```

```
Query Match 10.1%, Score 232.5; DB 17; Length 350;
Best local similarity 26.3%; Pred. No. 9e-09;
Matches 113; Conservative 57; Mismatches 153; Indels 107; Gaps 20;

QY 9 KFLGLGLVPLSLATIS-AGCWDKETTKEKSDNQNKQITDVSKISGLNKKSEIWA 67
DB 4 KFLGLG---LASVAVLSLACGRG-----A 26

QY 68 AKADANRKHFGILNAIVTAGTVDNSFNQSWEAIOQLGALTG-GRITVSVDSTAELECK 126
DB 27 SKGASAKTDLKAVMTVDGVDKSFNQSAMELQSGKEMGLOKGTGFYFQSTSESE 86

QY 127 YSSLIANTNKAVVTLSGQ--HGDAFTRWLKIPEKKOLFTEKNITIIIGIDWTDENTVPTG 184
DB 87 YA---TNLDTAVSGGYLIYIGIFA--LKDALAKAGDNGEVFVIID---DIEGKD 136
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QY 185 RYINLYKTEBAGMLAGYANASFLAKKPPSDPTKRSAL-VIGGISPATVDFIAGYLAGI 243
Db 137 NVASVTFAHDEAAIYLAGIAA-K-----TTTKTGVFGMEGTITTFEKGFBAGV 187
QY 244 KAMMLKSDKKTITTTKIEINLGF-----DVODSTKERLEQIASKDPSTLLAVAGPL 298
Db 188 KS-----VDDTIQVKVDYAGSFGDAKGTIAAQAAGAD--VIYQAAGGTG 233
QY 299 TEIFSDIIANONDR-----YLIGVDTQD--SLVYT-----KTKKKEFTSILKNLGSYFS 346
Db 234 AGVNEAKAIKESSEADKVVIGVDRQKDEGKITSODGEANFVLAASIKKGVKAQVL 293
QY 347 VLSDLYTKKSNRLNLAGFEFGKSAATVYLGIKDRFVDIADTSLGNDKKLATEALSEAKK 406
Db 294 INKQVADKK-----FPGK--TTYV-GLKGGVEIATT-----NVSKAIVAKIKEAKA 338
QY 407 EFEKTKTIP 416
Db 339 KIKSGDIKVP 348

RESULT 2

US-09-769-787-132
; Sequence 132, Application US/09769787
; Publication No. US20030091577A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hanebro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P2129WO
; CURRENT APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 132
; LENGTH: 350
; TYPE: PRF
; ORGANISM: Streptococcus pneumoniae
US-09-769-787-132

Query Match 9.7%; Score 223; DB 10; Length 350;
Best Local Similarity 24.8%; Pred. No. 4.5e-08;

Matches 110; Conservative 63; Mismatches 148; Indels 122; Gaps 22;

QY 1 MKKKIKMKNKFLGLGVPLSAIATIS-AGCWDKETTKEKSGADNQNKOITDVSKISGLVN 59
Db 1 MNKK-----QWTLGLIV-----AVALVGLAACNRSRNASSDVYTK----- 39
QY 60 ERKSEIMAAKADANKFGLMAIYTAGTVNDNSFNQSWALIQOLGA---LTGSEITSV 116
Db 40 -----AAIYDTGTGVDDKSFNOSAMEGLQAMGKEHNI,SKDNNGFTY 79
QY 117 DNSTAELE-----GKYSILANTKNVWVLSGFQGDAPFTMLKIKPENKOLFTEKNI 167
Db 80 FQSTSEADYANNLOQAAAGSTVILFGV-----GFALANNA-----VKDAKERTDILNY 125
QY 168 IILGIDWTDENVLPTRKYNLYKTEBAGMLAGYANASFLAKKPPSDPTKRSALVIGGG 227
Db 126 VLIDVDVLDQGV-----ASVTFADNESGYLAGYAAK-----TTTKQVGFVG 170
QY 228 I-SRAVDFIAGYLAGIYAMMLKSDKKTITTTKIEINLGFVDVODSTKERLEQIASKD 286
Db 171 ISESVISRFEAGFRAGV-----ASVDPISIKQVVDYAG-SFG-DAKAGKTIAAQAAGAD 223
QY 287 KPSTLLAAVAGPL-TEIFSDIIANONDR-----YLIGVDTQD--SLVYT-----KTKKKEFT 333
Db 224 ---IVQVAGGTGAGVFAEAKSLNESRPEKNEKVVIGVDRQDEAEGKITSKDGKESNFVL 280

QY 334 TSLIKNLGSYFSVLSDLYTKKSNRLNLAGFEFGKSAATVYLGIKDRFVDIADTSLGND 393
Db 281 VSTLKQVGTIVKDI-----SNKABERGEPPGQ---VIYSLKDGKVDLAIVNLSEEG 329
QY 394 KKLATEALSEAKKEFEKTKTIP 416
Db 330 KK-----AVEDAKAKILDGSVKVP 348

RESULT 3

US-10-451-337-6
; Sequence 6, Application US/10451337
; Publication No. US20040097706A1
; GENERAL INFORMATION:
; APPLICANT: SHIRE BIOCHEM INC.
; APPLICANT: MARTIN, Denise
; APPLICANT: BRODEUR, Bernard R.
; APPLICANT: HAMEL, Joee
; APPLICANT: RIOUX, Stephane
; APPLICANT: RHEAULT, Patrick
; TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS AND
; TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
; FILE REFERENCE: 12806-24PCT
; CURRENT APPLICATION NUMBER: US/10/451,337
; PRIOR FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: US 60/256,940
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 344
; TYPE: PRF
; ORGANISM: S. pyogenes
US-10-451-337-6

Query Match 9.6%; Score 221; DB 15; Length 344;
Best Local Similarity 26.4%; Pred. No. 6.1e-08;

Matches 115; Conservative 56; Mismatches 141; Indels 124; Gaps 23;

QY 9 KFLGLGVPLSAIATIS-AGCWDKETTKEKSGADNQNKOITDVSKISGLVNERKSEIMA 67
Db 3 KFLGL-----LASVAVLSLAACNKG-----A 25
QY 68 AKADANKFGLMAIYTAGTVNDNSFNQSWAL---QOLGALTGSEITSVDSSTAELE 124
Db 26 SKGASGKTDLKVMATVDTGVDKSFNOSAMEGQSGKEMGLQK---TGFDFQSTSE 82
QY 125 GKYSILANTKNVWVLSGFQ--HGDAPTRMLK-----IPENKOLFTEKNIITIIIGIDWTD 176
Db 83 SEVA---TMDLTVSGGYOLIYGIFA--LKDAIARAAGDGVKFYIIDIIEGKD-- 133
QY 177 TENYIPTRGVINLYKTEBAGMLAGYANASFLAKKPPSDPTKRSALVIGGISPATVDFI 236
Db 134 --NV-----ASVTFADHEAAIYLAGIAA-K-----TTTKTGVFGMEGTITTRF 176
QY 237 AGYLAGIKAMMLKNSDKKTITTTKIEINLGF-----DVODSTKERLEQIASKDKPSTL 291
Db 177 EGFEAGVKS-----VDDTIQVKVDYAGSFGDAKGTIAAQAAGAD--VIY 222
QY 292 LAVAGPLTEIFSDIIANON--DR-YLIGVDTQD--SLVYT-----KTKKKEFTSILKNL 340
Db 223 QAAAGTGAGVNEAIIKESSEADKVVIGVDRQKDEGKITSODGEANFVLAASIKK 282
QY 341 GYSVFSVLSDLYTKKSNRLNLAGFEFGKSAATVYLGIKDRFVDIADTSLGNDKKLATEA 400
Db 283 GKAVQILINKQVADK-----FPGK--TTYV-GLKGGVEIATT-----NVSKAIVAKA 326
QY 401 ISEAKKEFEKTKTIP 416
Db 327 IKEAKAKIKSGDIKVP 342

;; PRIOR FILING DATE: 2000-12-21
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 16
;; LENGTH: 330
;; TYPE: PRT
;; ORGANISM: S. pyogenes
US-10-451-337-16

Query Match 9.3%; Score 214.5; DB 15; Length 330;
Best Local Similarity 28.3%; Pred. No. 1.7e-07;
Matches 102; Conservative 46; Mismatches 143; Indels 69; Gaps 17;

QY 67 AAKADAKHFGALMAIYTAGTVNDNSFNOSWEAIOQLGALTG-GETSVDSSTAIEEG 125
DB 19 ASKGAAGAKTDLKAAMATDTGCVDDKSPNGSAMGLDSWGMELQKGTGTGYQSTSES 78
QY 126 KYSLANTNKNVWVLSGFG--HGDAFTRWLKIPEKNKILIGIDWTDTENVIPT 183
DB 79 EVA-----TNDTAVSGGYQLIYGIGA--LKDAIAKAGNDEGVKFIID----DIEGK 128
QY 184 GRYNLTYTEBEAGWLAGYANASFLAKKPSDPTKRSAL-VIGGISPATVDFIAGYIAG 242
DB 129 DNVAATVPADHEAAVYLAGIAAK-----TTKTITGVFGMEGTVITRFEKGEAG 179
QY 243 IKAMNLKNSDKTKITTDKIEINLGF-----DVQDSTKERLEQIAKDKPSTLLAAGP 297
DB 180 VKS-----VDDTIQVKVDYAGSFGDAKAGKTIAAQYAAAGAD--VIQAAAGT 225
QY 298 LTEIFSDIIANQDR-----YLIGVDTQ--SLVYT---KTKNKFSTILKNLGYSVF 345
DB 226 GAGVFNBAKAIINEKRSBADKVVWIGVDRDQDEGKYTSKDGKEANFVLASSIKGVKAVQ 285
QY 346 SVLSDLTYKKSNSKNLAGFPERGKKSATVYLGIKRPFVDIADTSLEGNDKLATPAISEAK 405
DB 286 LINKQVADK-----FPGK--TTVY-GLKDGVEIAT--NVSKEAVAKIIEAK 330

RESULT 10
US-10-451-337-42
;; Sequence 42, Application US/10451337
;; Publication No. US20040097706A1
;; GENERAL INFORMATION:
;; APPLICANT: SHIRE BIOCHEM INC.
;; APPLICANT: MARTIN, Denis
;; APPLICANT: BRODEUR, Bernard R.
;; APPLICANT: HAMEL, Josée
;; APPLICANT: RHEAULT, Patrick
;; APPLICANT: RHEAULT, Patrick
;; TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS AND
;; TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
;; FILE REFERENCE: 12806-24PCT
;; CURRENT APPLICATION NUMBER: US/10/451.337
;; CURRENT FILING DATE: 2003-11-18
;; PRIOR APPLICATION NUMBER: US 60/256,940
;; PRIOR FILING DATE: 2000-12-21
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 42
;; LENGTH: 330
;; TYPE: PRT
;; ORGANISM: Mouse
US-10-451-337-42

Query Match 9.3%; Score 214.5; DB 15; Length 330;
Best Local Similarity 28.3%; Pred. No. 1.7e-07;
Matches 102; Conservative 46; Mismatches 143; Indels 69; Gaps 17;
QY 67 AAKADAKHFGALMAIYTAGTVNDNSFNOSWEAIOQLGALTG-GETSVDSSTAIEEG 125
DB 19 ASKGAAGAKTDLKAAMATDTGCVDDKSPNGSAMGLDSWGMELQKGTGTGYQSTSES 78
QY 126 KYSLANTNKNVWVLSGFG--HGDAFTRWLKIPEKNKILIGIDWTDTENVIPT 183

DB 79 EVA-----TNDTAVSGGYQLIYGIGA--LKDAIAKAGNDEGVKFIID----DIEGK 128
QY 184 GRYNLTYTEBEAGWLAGYANASFLAKKPSDPTKRSAL-VIGGISPATVDFIAGYIAG 242
DB 129 DNVAATVPADHEAAVYLAGIAAK-----TTKTITGVFGMEGTVITRFEKGEAG 179
QY 243 IKAMNLKNSDKTKITTDKIEINLGF-----DVQDSTKERLEQIAKDKPSTLLAAGP 297
DB 180 VKS-----VDDTIQVKVDYAGSFGDAKAGKTIAAQYAAAGAD--VIQAAAGT 225
QY 298 LTEIFSDIIANQDR-----YLIGVDTQ--SLVYT---KTKNKFSTILKNLGYSVF 345
DB 226 GAGVFNBAKAIINEKRSBADKVVWIGVDRDQDEGKYTSKDGKEANFVLASSIKGVKAVQ 285
QY 346 SVLSDLTYKKSNSKNLAGFPERGKKSATVYLGIKRPFVDIADTSLEGNDKLATPAISEAK 405
DB 286 LINKQVADK-----FPGK--TTVY-GLKDGVEIAT--NVSKEAVAKIIEAK 330

RESULT 11
US-09-765-272-8
;; Sequence 8, Application US/09765272
;; Patent No. US20020061545A1
;; GENERAL INFORMATION:
;; APPLICANT: Choi et. al.
;; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
;; NUMBER OF SEQUENCES: 452
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/765.272
;; FILING DATE: 22-Jan-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/961,083
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brookes, A. Anders
;; REGISTRATION NUMBER: 36,373
;; REFERENCE/DOCKET NUMBER: PB340P2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8512
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 328 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-765-272-8

Query Match 8.8%; Score 203; DB 9; Length 328;
Best Local Similarity 25.7%; Pred. No. 1.2e-06;
Matches 98; Conservative 56; Mismatches 144; Indels 84; Gaps 19;
QY 61 RKSEIMAKKDHGFGALMAIYTAGTVNDNSFNOSWEAIOQLGA---LTGETSVSD 117
DB 3 RSRNNAASSSDVK---TKAAIIVDTDTGCVDDKSPNGSAMGLDSWGMELQKGTGTGYQSTSES 78
QY 118 SSTAIE-----GKYSANTNKNVWVLSGFGHGDFTRWLKIPEKNKILIGIDWTDTENVIPT 168

```
Db 59 QSTSEADYANNLQQAAGSYNLIFGV-----GFLANNA-----VDAKKEHTDLNLYV 104
Qy 169 ILIGDMTDTEENVLPTRGRYINLTYTEAGWLAGYANASFLAKFPSPDPTKSAIVIGGGI 228
Db 105 LIDVIDYDQKQV-----ASVTFADNBSGYLAGVAANK-----TTTKQVGFVGGI 149
Qy 229 -SPAVIDFIAGYLAGIKAMNLKNSDKTKYITTDKIEINLGFVDVDTSTKERLEQIASDK 287
Db 150 ESEVISRFEAGFKAGV-----ASVDPSIKVQVDYAG-SFG-DAAKGKTIAAQYAAAGAD- 201
Qy 288 PSTLLAAGPL-TEIFSDIIANQDR-----YLIGVDTDSL--VYT-----KTKKKEFT 334
Db 202 --IVYQVAGTGAGVFAAKSLNESRPENEKVWVIGVDRDQABGKTYSDGKESNPLYV 259
Qy 335 SILKMLGYSVFSLDYTKKSNRNLAGFEFGKSAATVYLGIDRFVADIADTSLEGNDK 394
Db 260 STLQVGTTVKDI-----SNKAEREFPFGCG--VIVYSLDKGVDLAVTNLSEBGK 308
Qy 395 KLATEAISEAKKEFEKTKTIP 416
Db 309 K---AVEDAKAKILDSGVKVP 326
```

RESULT 12

```
US-10-451-337-8
; Sequence 8, Application US/10451337
; Publication No. US20040097706A1
; GENERAL INFORMATION:
; APPLICANT: SHIRE BIOCHEM INC.
; APPLICANT: MARTIN, Denis
; APPLICANT: BRODEUR, Bernard R.
; APPLICANT: HAMEL, Josee
; APPLICANT: RIOUX, Stephane
; APPLICANT: RHEAULT, Patrick
; TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS AND
; TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
; FILE REFERENCE: 12806-24PCT
; CURRENT APPLICATION NUMBER: US/10/451,337
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: US 60/256,940
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 347
; TYPE: PRT
; ORGANISM: S. pyogenes
US-10-451-337-8
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```
Query Match 8.2%; Score 188.5; DB 15; Length 347;
Best Local Similarity 25.7%; Pred. No. 1.5e-05;
Matches 113; Conservative 59; Mismatches 150; Indels 117; Gaps 25;

Qy 1 MKKKIKNNKFGGLVPLSLAIATISAGCWDKETTKEKSADNONKQITDVSKISGLVNE 60
Db 1 MNKKV-----MSLGLV--STALFTL-GGC-----TNSAKQTTDNS----- 33
Qy 61 RKSEIMAKADANKHFGILNMAIVTAGGVNDNSFNQSGMEALQOLG--ALTGE---I 113
Db 34 -----LKIAMITNQIGIDKSFNQSAWEGLOQWKGKENTLEKKGXYDF 76
Qy 114 TSVDSS--TAELEKYSLSLANTKNVWVLSGFQHGDAFTR-WLKIPENKQLFTEKNIIIL 170
Db 77 QSANESFETTNLE--SAVTNGYNLVFGI-GFPLHDAVEKVAANNPDNH--FAIVDVIK 130
Qy 171 GIDWTDTEENVLPTRGRYINLTYTEBAGWLAGYANASFLAKFPSPDPTKSAIVIGGGISP 230
Db 131 G-----QKNV-----ASITFSDHEAAVLAGVAANK-----TTTKQVGFV-GGMEGD 171
Qy 231 AVTDFIAGYLAGIKAMNLKNSDKTKYITTDKIEINLGFVDVDTSTKERLEQIASDKRST 290
Db 172 VVKRFEKGFAGVSV-----DTIKVRAVYAGSPADAAGKGTIAAQYABGADV 221
```

```
Qy 291 LL-AVAGPLTEIFSDIIANQDR-----YLIGVDTDSL--VYT-----KTKKKEFTSIL 337
Db 222 IYHAAAGTGAGVFSEAKSINEKREEDKVVWVIGVDRDQSBGKTYTKDGSANFVLTSSI 281
Qy 338 KNLGYSVFSVLSLDYTKKSNRNLAGFEFGKSAATVYLGIDRFVADIADTSLEGNDKLA 397
Db 282 KEVGKALVKA-----VITSBD-----QFPGGQITTF-GKEGGVSLTTDALTDYTK-- 328
Qy 398 TEAISEAKKEFEKTKTIP 416
Db 329 --AIEAAKKAIIIEGTITVP 345
```

RESULT 13

```
US-10-474-792-180
; Sequence 180, Application US/10474792
; Publication No. US20040236072A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Stephen
; APPLICANT: Zagursky, Robert
; APPLICANT: Nickbarg, Elliot
; APPLICANT: Winter, Louie
; TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
; FILE REFERENCE: AM 100399
; CURRENT APPLICATION NUMBER: US/10/474,792
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 180
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-474-792-180
```

```
Query Match 8.2%; Score 188.5; DB 17; Length 347;
Best Local Similarity 25.7%; Pred. No. 1.5e-05;
Matches 113; Conservative 59; Mismatches 150; Indels 117; Gaps 25;

Qy 1 MKKKIKNNKFGGLVPLSLAIATISAGCWDKETTKEKSADNONKQITDVSKISGLVNE 60
Db 1 MNKKV-----MSLGLV--STALFTL-GGC-----TNSAKQTTDNS----- 33
Qy 61 RKSEIMAKADANKHFGILNMAIVTAGGVNDNSFNQSGMEALQOLG--ALTGE---I 113
Db 34 -----LKIAMITNQIGIDKSFNQSAWEGLOQWKGKENTLEKKGXYDF 76
Qy 114 TSVDSS--TAELEKYSLSLANTKNVWVLSGFQHGDAFTR-WLKIPENKQLFTEKNIIIL 170
Db 77 QSANESFETTNLE--SAVTNGYNLVFGI-GFPLHDAVEKVAANNPDNH--FAIVDVIK 130
Qy 171 GIDWTDTEENVLPTRGRYINLTYTEBAGWLAGYANASFLAKFPSPDPTKSAIVIGGGISP 230
Db 131 G-----QKNV-----ASITFSDHEAAVLAGVAANK-----TTTKQVGFV-GGMEGD 171
Qy 231 AVTDFIAGYLAGIKAMNLKNSDKTKYITTDKIEINLGFVDVDTSTKERLEQIASDKRST 290
Db 172 VVKRFEKGFAGVSV-----DTIKVRAVYAGSPADAAGKGTIAAQYABGADV 221
Qy 291 LL-AVAGPLTEIFSDIIANQDR-----YLIGVDTDSL--VYT-----KTKKKEFTSIL 337
Db 222 IYHAAAGTGAGVFSEAKSINEKREEDKVVWVIGVDRDQSBGKTYTKDGSANFVLTSSI 281
Qy 338 KNLGYSVFSVLSLDYTKKSNRNLAGFEFGKSAATVYLGIDRFVADIADTSLEGNDKLA 397
Db 282 KEVGKALVKA-----VITSBD-----QFPGGQITTF-GKEGGVSLTTDALTDYTK-- 328
Qy 398 TEAISEAKKEFEKTKTIP 416
Db 329 --AIEAAKKAIIIEGTITVP 345

RESULT 14
```


US-09-071-035-80
Sequence 80, Application US/09071035
Publication No. US20020045737A1
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071.035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-80

Query Match 7.9%; Score 182; DB 9; Length 339;
Best Local Similarity 25.4%; Pred. No. 4.4e-05;
Matches 104; Conservative 51; Mismatches 139; Indels 116; Gaps 20;

QY 61 RKSEIMAKADANKHFGILNMAIVTAGTVNDNSFNQSSWEAIOQLG--LTGE----- 112
DB 7 KTASGGGKGDA---AHSAVIITDTGGVDKSFQSSWEGLOAMGKEHDLPEGSKGYAY 62
QY 113 ITSVDSS--TALEGGKSSSLANTNKNVWVLSGFQHGDAFTRWLKIPEKQOLFTEKNIIL 170
DB 63 IQSNDAADYTNIDQAVSSKFNITFGI---GYLLKDA-----ISSAADNPPTNFVLI 112
QY 171 GIDWTDENVIPTRGYINLFTYTEAGWLAGYANASFLAKKFPSPDPTKSAIVIGGIGSP 230
DB 113 DDQIDGKKNV-----VSATFRDNEAAYLAGVAAA-----NETKTNVGVGGESE 157
QY 231 AVTD-FLAGYLAGIKAMNKNKSDKTKITTDKIEINLGFVDVDTSTYERLEQIASKDKPS 289
DB 158 VVIDRFQAGFEKGV-ADAKELGKEITVDT-----KYAASFADPA 196
QY 290 TLLAVAGPLTEIFEDII-----ANQNR-YLIGVDTDQSL--VYT 326
DB 197 KGKLAAMVONGVILIFHASGATGCGVFOEAKDLNESGSDKVMWIVGDRDQADGKY- 255
QY 327 KTK-----NKEFTSLIKMLGYSVSVLSDLTYKKSNSHNLGFEFGKKSATVYIGIKDRF 381
DB 256 KTKGKKEKNTFLITSLKGVTAODIANRALEDK-----PFGSEHLVY-GLKGG 304
QY 382 VDIADTSLGENDKCLATEAISEAKKEFEKTKTTPAEVVRKTLTEIPEMD 431
DB 305 VDLTDTGYL--NDKT-----KEAVTAKDKVIGSDVVKVEKPE 339

RESULT 15
US-10-206-576-80
Sequence 80, Application US/10206576
Publication No. US20030017495A1
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206.576
FILING DATE: 29-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/071.035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046.655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044.031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066.009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB369P1D1
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-206-576-80

Query Match 7.9%; Score 182; DB 14; Length 339;
Best Local Similarity 25.4%; Pred. No. 4.4e-05;
Matches 104; Conservative 51; Mismatches 139; Indels 116; Gaps 20;

QY 61 RKSEIMAKADANKHFGILNMAIVTAGTVNDNSFNQSSWEAIOQLG--LTGE----- 112
DB 7 KTASGGGKGDA---AHSAVIITDTGGVDKSFQSSWEGLOAMGKEHDLPEGSKGYAY 62
QY 113 ITSVDSS--TALEGGKSSSLANTNKNVWVLSGFQHGDAFTRWLKIPEKQOLFTEKNIIL 170
DB 63 IQSNDAADYTNIDQAVSSKFNITFGI---GYLLKDA-----ISSAADNPPTNFVLI 112
QY 171 GIDWTDENVIPTRGYINLFTYTEAGWLAGYANASFLAKKFPSPDPTKSAIVIGGIGSP 230
DB 113 DDQIDGKKNV-----VSATFRDNEAAYLAGVAAA-----NETKTNVGVGGESE 157
QY 231 AVTD-FLAGYLAGIKAMNKNKSDKTKITTDKIEINLGFVDVDTSTYERLEQIASKDKPS 289
DB 158 VVIDRFQAGFEKGV-ADAKELGKEITVDT-----KYAASFADPA 196
QY 290 TLLAVAGPLTEIFEDII-----ANQNR-YLIGVDTDQSL--VYT 326
DB 197 KGKLAAMVONGVILIFHASGATGCGVFOEAKDLNESGSDKVMWIVGDRDQADGKY- 255

Oy 327 KTK-----NKFFTSILKNLGYVFSVLSLDYTKKSNRNLAGFERGKSATVYLGIKDRF 381
Db 256 KTKDGEKEDNFTLTSTLKGVTAVODIANRALEDK-----FPGGEHLVY-GLKXDG 304
Oy 382 VDIADTSLGNDKKLATEAISEAKKEPEKTKTTPAEVRKTLRIPEMPD 431
Db 305 VDLTDGYL--NDKT-----KEAVKTAADKVIISGDVKVPEKPE 339

Search completed: December 18, 2004, 01:44:02
Job time : 106.236 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 18, 2004, 01:15:13 ; Search time 27.349 Seconds
(without alignments)
1586.669 Million cell updates/sec

Title: US-09-676-249D-2

Perfect score: 2299

Sequence: 1 MKKKIKWKKFLGLVLPPLS.....KQPDKQESLDKLTIDINKN 451

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	554.5	24.1	461	2 B90555	ABC transporter xy
2	223	9.7	350	2 G95097	lipoprotein lipor
3	219	9.5	374	2 G97965	conserved hypotet
4	207	9.0	350	2 F86804	basic membrane pro
5	195.5	8.5	357	2 D96986	probable lipoprote
6	187.5	8.2	516	2 C82946	hypothetical prote
7	185.5	8.1	350	1 C70009	ABC transporter (l
8	182	7.9	353	1 H71340	membrane lipoprote
9	181.5	7.9	359	2 F72418	basic membrane pro
10	178	7.7	341	2 E70147	basic membrane lip
11	174	7.6	357	2 AH1610	CD4+ T cell-stimul
12	169.5	7.4	360	2 H70147	basic membrane pro
13	169	7.4	357	2 AD1248	CD4+ T cell-stimul
14	168.5	7.3	525	2 C82914	conserved hypotet
15	164	7.1	524	2 D82944	hypothetical membr
16	162	7.0	339	2 F70147	basic membrane pro
17	156.5	6.8	591	2 D64204	membrane lipoprote
18	147	6.4	353	2 G70147	basic membrane pro
19	143.5	6.2	384	2 T40867	hypothetical prote
20	141.5	6.2	539	2 D82886	conserved hypotet
21	141	6.1	379	2 H75318	membrane lipoprote
22	140.5	6.1	337	2 AH2591	membrane lipoprote
23	140.5	6.1	337	2 B97374	Deinococcus radiod
24	132	5.7	547	2 E29504	mercury(II) reduct
25	132	5.7	657	2 S73428	probable lipoprote
26	130	5.7	484	2 B90524	hypothetical prote
27	129.5	5.6	1140	2 S73786	hypothetical prote
28	129.5	5.6	1558	2 B71603	REBA-H3 antigen pr
29	127.5	5.5	763	2 A82863	hypothetical prote

30	127	5.5	349	2 F84246	hypothetical prote
31	126	5.5	326	2 G95857	hypothetical prote
32	125	5.4	1635	2 A10452	hemolysin lipoprote
33	124.5	5.4	556	2 H82301	peptide ABC transp
34	124.5	5.4	2269	2 T28677	thoxytry protein -
35	123.5	5.4	322	2 F84236	ABC transporter (l
36	123.5	5.4	626	2 C25035	colicin Ia - Esche
37	123.5	5.4	1031	2 C81302	probable type I si
38	123.5	5.4	1223	2 E88451	protein K10D2.1 (l
39	122.5	5.3	553	1 SMEBH1	flagellar hook-aaa
40	122.5	5.3	553	2 AH0640	flagellar hook-aaa
41	122.5	5.3	2285	2 T12796	probable transglyc
42	122.5	5.3	2346	2 T13829	tyr homolog - trui
43	121	5.3	1546	2 G90603	lipoprotein (import
44	119.5	5.2	350	2 F70139	exported protein (
45	119.5	5.2	627	2 A41609	dnak-type molecule

ALIGNMENTS

RESULT 1

B90555 ABC transporter xylose-binding lipoprotein [imported] - Mycoplasma pulmonis (strain UAB

C/Species: Mycoplasma pulmonis

C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C/Accession: B90555

R/Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A/Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm

A/Reference number: A99512; MUID:21267165; PMID:11353084

A/Accession: B90555

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-461 <KOR>

A/Cross-References: UNIPROT:Q96QL5; GB:AL445566; PID:G14089760; PIDN:CAC13519.1; GSPDB:G:

A/Experimental source: strain UAB CTIP

C/Genetics:

A/Gene: MYPV 3460

A/Genetic code: SGC3

Query Match	24.1%	Score 554.5;	DB 2;	Length 461;
Best Local Similarity	30.3%	Pred. No. 2.6e-26;		
Matches 140;	Conservative 88;	Mismatches 175;	Indels 59;	Gaps 13;
Qy	5	IKMKFLGLVLPPLSAITISAGCMDEKTKKESKDNQNKOT--DVSKISLVNER- 61		
Db	1	MKLNR--KLPSILPVAALALALPPTF-----VSCAQNPVKTNLSKLTDLSSQKE 51		
Qy	62	-----KSEIMAKADANKHFGIANNAIYTAGGTVDNSFNQSSWEAIOQALTGGEI 113		
Db	52	VTEYQKIVENKIKQASLEFQK-----VVLITADNDIDKSFNQVYSQKTLKQFVDKAY 106		
Qy	114	TS-----VDSSTABLEGKYSLSIANTNNKVVWVLSGFQHDAPTRWLKIPENK 159		
Db	107	KSQKAEANGHKLNDYINSAVKDLQNYKVALDRGYTTLITGRQOENIEINFENDENL 166		
Qy	160	QLPTEKNIILIGITWPTEN-VIPTEGYINLTYTTERACMLAGANMSFLAKKPPSDPTK 218		
Db	167	RRFENKVKIIGVMAWPNANSKIPQGLSILFLPTEBAGWQAGVASADFGTKYANNEAK 226		
Qy	219	RSATVIGGTSIPATDFIAGLAGIKAMN--LKNSDKTKITTKIKIINLGFQVDTSTK 276		
Db	227	RAIAPFGGDPAGATDLDNGFFBIRKAMNSEAEANANKVKI VSNLVLDIGF-IPNKK 285		
Qy	277	ERLEQIASKDKPSTLLAVAGPLTEIFSDIT--ANQDRYLIGVTDQSLVYTKKKEP 333		
Db	286	EVANVYETGKSTSLPVAQPFVGVVDVLRKQTSDDRFVGVDTQDSLFTDSKRF 345		
Qy	334	TSILKNIIGYSVFSVLSPLYT-----KKSNSNLAGFGRGKSAVYVIGIKORFYDIA 385		
Db	346	TSIVKNIAPFYQILLALLTLTDEESVILKGNDFKLS---NPNKLVKKGSLAKFVNIT 402		

Qy 386 DTSLGNDKLTATEAISA--KKEFEKTKTTPAEVKTIE 425
Db 403 KSRVKSIXTOADSTIQKALDKMANPNSSKIEKEMTNGDLE 444

RESULT 2

G95097

110proteins [imported] - Streptococcus pneumoniae (strain TIGR4)

C/Species: Streptococcus pneumoniae

C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C/Accession: G95097

R:Terrellin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayem, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001

A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A/Reference number: A95000; MUID:21357209; PMID:11463916

A/Accession: G95097

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-350 <KUR>

A/Cross-references: UNIPROT:Q97RH0; GB:AE005672; PIDN:AAK74976.1; PID:g14972319; GSPDB:G

A/Experimental source: strain TIGR4

C/Genetics:

A/Gene: SP0845

C/Superfamily: ABC transporter yuFn

Query Match 9.7%; Score 223; DB 2; Length 350;

Best Local Similarity 24.8%; Pred. No. 2.4e-06;

Matches 110; Conservative 63; Mismatches 148; Indels 122; Gaps 22;

Qy 1 MKKKIKNNKFLGLVPLSLAIAITIS-AGCWDKETTKEKSADNQNKOITDVSKISGLVN 59

Db 1 MNKK---QWLGIGLV---AVALVGLAACGRRSSRNAASSDVYTK----- 39

Qy 60 ERKSEIMAAKADANKHFLNMAIYTAGTVNDNSFNQSWEAIIQOLGA---LTGGEITSV 116

Db 40 -----AAIVTDGVDKDSFQSGAMEGLQAMGKEHNLSDKNGFTY 79

Qy 117 DSTSLAELE-----GKYSGLANTNNKVVWVLSFGHDAFTRWLKIPEKOLPTEKNI 167

Db 80 FQSTSEADYANNLQQAAGSYNLIFGV-----GFLANNA-----YKDAKERTDILNY 125

Qy 168 IILGIDWTDENVIPTGRYINLTYKTEBAGWLAGYANASFLAKKPPSDPTKRSALVIGGG 227

Db 126 VLIDDIVIKDQKNV-----ASVTFADNESGYLAGVAAAK-----TTTKQGVFGG 170

Qy 228 I-SPAIVDFIAGYLAGIRANMLKNSDKTKITTDKIEINLGFVDQDTSTKERLEQIASKD 286

Db 171 IESEVISRFEAGFRAGV-----ASVDPISIKQVDVYAG-SFG-DAAKGTIAAQAAGAD 223

Qy 287 KPSTLLAAVGPL-TEIFSDIIANQNDR-----YLIGVDTQSL-VYT-----KTQKKEF 333

Db 224 ---IVYQVAGGTGAGVFAEAKSLNESRPNKRWVIGDRQBEAGKTSKDGKESNFVL 280

Qy 334 TSILKNIQSVFVSLDLYTKKSNRLAGFEFGKSAATVYLGIDRFVDIADTSLGND 393

Db 281 VSTLKQVGTIVKDI-----SNKAERGEPGGQ---VIYSLKDKVDLAATNLSEEG 329

Qy 394 KKATLTAISEAKKEFEKTKTIP 416

Db 330 KK---AVEDAKAKILDSGVKVP 348

RESULT 3

C97965

Conserved hypothetical protein spr0747 [imported] - Streptococcus pneumoniae (strain R6)

C/Species: Streptococcus pneumoniae

C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C/Accession: C97965

R:Hokings, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M

Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234

A/Accession: C97965

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-374 <KUR>

A/Cross-references: UNIPROT:Q8DQC2; GB:AE007317; PIDN:AAK99551.1; PID:g15458340; GSPDB:G

C/Genetics:

A/Gene: spr0747

Query Match 9.5%; Score 219; DB 2; Length 374;

Best Local Similarity 24.6%; Pred. No. 4.7e-06;

Matches 109; Conservative 62; Mismatches 150; Indels 122; Gaps 21;

Qy 1 MKKKIKNNKFLGLVPLSLAIAITIS-AGCWDKETTKEKSADNQNKOITDVSKISGLVN 59

Db 25 MNKK---QWLGIGLV---AVALVGLAACGRRSSRNAASSDVYTK----- 63

Qy 60 ERKSEIMAAKADANKHFLNMAIYTAGTVNDNSFNQSWEAIIQOLGA---LTGGEITSV 116

Db 64 -----AAIVTDGVDKDSFQSGAMEGLQAMGKEHNLSDKNGFTY 103

Qy 117 DSTSLAELE-----GKYSGLANTNNKVVWVLSFGHDAFTRWLKIPEKOLPTEKNI 167

Db 104 FQSTSEADYANNLQQAAGSYNLIFGV-----GFLANNA-----YKDAKERTDILNY 149

Qy 168 IILGIDWTDENVIPTGRYINLTYKTEBAGWLAGYANASFLAKKPPSDPTKRSALVIGGG 227

Db 150 VLIDDIVIKDQKNV-----ASVTFADNESGYLAGVAAAK-----TTTKQGVFGG 194

Qy 228 I-SPAIVDFIAGYLAGIRANMLKNSDKTKITTDKIEINLGFVDQDTSTKERLEQIASKD 286

Db 195 IESEVISRFEAGFRAGV-----ASVDPISIKQVDVYAG-SFG-DAAKGTIAAQAAGAD 247

Qy 287 KPSTLLAAVGPL-TEIFSDIIANQNDR-----YLIGVDTQSL-VYT-----KTQKKEF 333

Db 248 ---IVYQVAGGTGAGVFAEAKSLNESRPNKRWVIGDRQBEAGKTSKDGKESNFVL 304

Qy 334 TSILKNIQSVFVSLDLYTKKSNRLAGFEFGKSAATVYLGIDRFVDIADTSLGND 393

Db 305 VSTLKQVGTIVKDI-----SNKAERGEPGGQ---VIYSLKDKVDLAATNLSEEG 353

Qy 394 KKATLTAISEAKKEFEKTKTIP 416

Db 354 KK---AVEDAKAKILDSGVKVP 372

RESULT 4

F86804

basic membrane protein A [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C/Species: Lactococcus lactis subsp. lactis

C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C/Accession: F86804

R:Botolin, A.; Winkler, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp

A/Reference number: A86625; MUID:21235186; PMID:11337471

A/Accession: F86804

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-350 <STO>

A/Cross-references: UNIPROT:Q9CFM9; GB:AE005176; PID:g12724428; PIDN:AAK05536.1; GSPDB:G

C/Genetics:

A/Gene: bmpA

Query Match 9.0%; Score 207; DB 2; Length 350;
Best Local Similarity 24.2%; Pred. No. 2.3e-05;
Matches 107; Conservative 62; Mismatches 156; Indels 118; Gaps 20;

QY 1 MKKKIKNNKFLGLVPELPSAIAATIS---AGCWDKETTKESKADNONKOITDVSKISG 56
 DB 1 MKKR-----VIAVSLALASVAVLAGCSHDAAGSGK----- 32
 QY 57 LVNERKSEIMAAKADANKHFGNLMAIYTAGTVDNDSFNOSSEWALIOQLGALTG-----G 111
 DB 33 -----AKTD-----LKAALIVTEIGVNDRSFNOSAMEGLQSGWKENNLKKGTG 75
 QY 112 EITSVDSSTAELEBKYSGLANTNNVWVLGSGFHGDAFTRLKIPENKQLTENKIIILG 171
 DB 76 YTFPOSASADYTTNNVSAEQGYKLEFGTFSIQDATSAAK---NN---PKSNFVIWD 129
 QY 172 IDWTDENVIPGTGRYINLYTKTEBAGMLAGYANASFLAKKPPSPDKRSAL-VIGGGISP 230
 DB 130 SVIQDQGNV-----ASATFADNESAVLAGVAALK-----ATKNKIGFICGMQSD 174
 QY 231 AVTDFIAGYLAGIYANMLKNSDKKTKITTDKIEINLGFVDVDTSTKERLEQIASKDPST 290
 DB 175 VITFEKGYEAGAKSVN-----PDIKVDVQVAGSFSDAKAGKTIAAAMYAGADVD 224
 QY 291 LNAVAGPL-TEIFSDIIA-----NONDR-VLIGVDTQSLV--VT---KTKNKFPTSIL 337
 DB 225 VYOCAGGVGTGVFEAKALNSTKNEADKVVIVGDQDEYLGKTKSKDGKDSNFWLVSTI 284
 QY 338 KNLGYSVFVSLDLYTKKSNRNLAG--FEFGKSAATVYLGIKDRFYDIADTSLGENDKK 395
 DB 285 KEVG---NVKQDIADTKKQKFGGTIVYIDLNGGVNIGL-----DSANSEIK----- 330
 QY 396 LATEAISEAKKEFEKTKTTPAE 418
 DB 331 ---DAVAKAKADIIDGKITVPSK 350
 RESULT 5
 D96986
 Probable: lipoprotein, Med/BMP family [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C:Accession: D96986
 R:Kolling, J.; Betton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183: 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1c
 A:Reference number: A96900; MUID:21359325; PMID:2159325
 A:Accession: D96986
 A:Stature: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <KUR>
 A:Cross-references: UNIPROT:Q97L60; GB:AE001437; PIDN:AAK78679.1; PID:G15023581; GSPDB:C
 C:Experimental source: Clostridium acetobutylicum ATCC624
 C:Genetic: CAC0702

Query Match 8.5%; Score 195.5; DB 2; Length 357;
 Best Local Similarity 22.3%; Pred. No. 0.00012;
 Matches 100; Conservative 72; Mismatches 156; Indels 121; Gaps 20;

QY 1 MKKKIKNNKFLGLVPELPSAIAATISAGCWDKETTKESKADNONKOITDVSKISGLVNE 60
 DB 2 IKKKT-----IAILTTVMIVAGIFAGC-----SSTSSGSGNS 33
 QY 61 RKSEIMAAKADANKHFGNLMAIYTAGTVDNDSFNOSSEWALIOQLGALTGSEITSVDSST 120
 DB 34 K-----DTK-----VKGLSTDEGLNDKSNQAGDEQIKKAAXSYSDYRAISEKK 81
 QY 121 A-ELEGKYSGLANTNNVWVLGSGFHGDAF-TRMLKIPENKQLTENKIIILG 171
 DB 82 KDQVQPNLQSLIDNDSLDLVFGVGYQMDLDTIAKKYDPKFAIIDAADYKQPKNI----- 137
 QY 172 IDWTDENVIPGTGRYINLYTKTEBAGMLAGYANASFLAKKPPSPDKRSAL-VIGGGISP 230
 DB 138 -----MSLVFKQSGSFLMG-----VLAGKM-----TKTNKIGFVGSKQOP 173

QY 231 AVTDFIAGYLAGIYANMLKNSDKKTKITTDKIEINLGFVDVDTST-KERLEQIASKDKPS 289
 DB 174 LNKFLISGLYIAGAKTVN-----PNITVEK---NNTYNDSPISKGEVATSLVNGGCDI 223
 QY 290 TLLAVAPLLEIISDIANONDR-----YLIGVDTQSLVYTKTKNKFPTSILKNLGVSFV 345
 DB 224 VYHAGAGIGVF-DVAKSIRDOGDQVMAIGVQDAAGLPKXADVILTSMVKRVDIATY 282
 QY 346 SVLSDLVTKKSNRNLAGFEFGKSAATVYLGIKDRFYDIADTSLGENDKLTATEAISEAK 405
 DB 283 NTVKDLVKGK-----FEFGKVES---FGLEDYGVAVPTS---NKIVPSVSLVD 328
 QY 406 K-----EFEKTKTTPAEVR 421
 DB 329 KYKKAIDGKIIVPDVDTKQTFKTDQIK 357

RESULT 6
 C82946
 Hypothetical protein U0012 [imported] - Ureaplasma urealyticum
 C:Species: Ureaplasma urealyticum
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: C82946
 R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Casseil, G.H.
 submitted to GenBank, February 2000
 A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
 A:Reference number: A82870
 A:Accession: C82946
 A:Stature: preliminary
 A:Molecule type: DNA
 A:Residues: 1-516 <GLA>
 A:Cross-references: GB:AE002100; GB:AF222894; NID:G6898946; PIDN:AAF30417.1; GSPDB:GN001;
 C:Experimental source: serovar 3, biovar 1
 C:Genetic: U0012
 A:Gene: U0012
 A:Genetic code: SGC3

Query Match 8.2%; Score 187.5; DB 2; Length 516;
 Best Local Similarity 23.3%; Pred. No. 0.00061;
 Matches 117; Conservative 67; Mismatches 167; Indels 151; Gaps 25;

QY 1 MKKKIKNNKFLGLVPELPSAIAATISAGCWDKETTKESKADNONKOITDVSKISGLVNE 60
 DB 1 MKKLNKVLFLAIGSVPALGTIIIVATSCYQKSTL----- 35
 QY 61 RKSEIMAAKADANKHFGNLMAIYTAGTVDNDSFNOSSEWALIOQLGALTGSEITSVDSST 120
 DB 36 -----NYSQPYW-----TSPTSDD 49
 QY 121 AE-LEGKYSGLANTNNVWVLGSGFHGDAFTRLKIPENKQ--LFTK-----NIIIL--G 171
 DB 50 DEGRQTKSKMASGKALMLPGYH-----PERQNALVNDKFPBNLIALILDG 99
 QY 172 IDWTDENVIPGT--RYINLYTKTEBAGMLAGYANASFLAKK--PSPDKRSALVIIG 226
 DB 100 VYNNDNKAEPYKGAADVAFYKVDAAFLGIAAAYMLNSQAVFGAD-----NKLTVGG 155
 QY 227 --GISPA-VNDFIAGYLAGIYANMLKNSDKKTK--ITTDKIEINL-----GFD 269
 DB 156 YVGINAKNTNNYLAGFPLGVKMAEKKDKNIQOEGTQETKQWVNEQVYASSESSAGFQ 215
 QY 270 VQDSTKERLEQIASKDKPSLTLAVAGPLTEI-FSDIIANONDRY-LIGVD---TDQSL 323
 DB 216 SDSANAKKIIOELITTK-ADLILPVALPQVGIANTTEALITSHNVGVIQVDEIENQAI 274
 QY 324 VYTKNKFPTSIL--KNLGYSVFVLS--DLVTKKSNRNLAGFEFGKSAATVYLG- 377
 DB 275 --NKTKDKFINTHLSGKN--GVIRFSITKRLDTITLLENALIGESLSKSDDIVIGSE 331
 QY 378 ---KDRF---VDIADTSLG-----NDKLTATEAISEAKKEFEKTKTTPAE 418
 DB 332 IDPKDKYKLGIVNTVGNLSDGVGISPSAHYVIDAFNLACTNOSDKVSTYDELVNKLTND 391

QY 419 EVKTLTEIPENPKQPKQES 440
Db 392 DLFKTLDKKPVVDGYLDVKKET 413

RESULT 7

ABC transporter (lipoprotein) homolog yuFn - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: C70009
R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillette, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Galle
lech, J.; Harwood, C.R.; Henaut, A.; Hiltbert, H.; Holstappel, S.; Hosono, S.; Hullo, M.F.
koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinis,
A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A.; Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpiltra, P.; Togononi, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumestein, E.; Yoshikawa, H.; Dancin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: C70009
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-350 <KUN>
A:Cross-references: UNIPROT:005252; GB:Z99120; GB:AL009126; NID:92635613; PIDN:CAB15143.
A:Experimental source: strain 168
C:Genetics:
A:Gene: yuFn
C:Superfamily: ABC transporter yuFn

Query Match 8.1%; Score 185.5; DB 1; Length 350;
Best Local Similarity 24.8%; Pred. No. 0.00046;
Matches 106; Conservative 61; Mismatches 149; Indels 111; Gaps 21;

QY 21 AIAITSACMDKETTKEKSDNKNQKQITDVSKISGLVNEKSEIMAKADANRFGIUM 80
Db 6 AAGTILGACGNSE--KSSGSGEGKXK-----RSV 32
QY 81 AIVTAGTVNNDNSFNQSSWEAIIQGLGALTG-----GEITSVDSSTAELEGYSIANTN 134
Db 33 AMVTDVGVDDKSPFQSGMEGIQARGKNGLKKGKNGDYLDOSKSDADYTTNMLAKEN 92
QY 135 KNWVLVSGFHGDFAFTRWLKIPENKQIFTEKNIIILGID-WTDTENVIPTRGYINLTYYKT 193
Db 93 FDLIVGVGLMEDSIS--EIADQR-----KNTNPAIIDAVIDKONV-----ASITPKE 138
QY 194 BEAGMLAYANASFLAKKPPSDPTKSAI-VIGGISISAVNDFIAGYLAGIKAMLNKSD 252
Db 139 QEGSLVAVAAAL-----SSKSGKIGFVGMESELKKFEVGFAGVAVAPK--- 186
QY 253 KKTITTKRIEINLGFVDVT--STKERLEQIASDKPSTLLAVAPL-TEIFSDIIAN- 308
Db 237 KKEDPKRDVWVYGVADQYAEQVGEVDNVTLTSMVK-----KVDYVEDV-TRKASDGK 291
QY 309 -----QNDRYILGVDTQ--SLVYTKTRNKFSTILKNLGYSVFSLDLYTKKSNRN 360
Db 237 KKEDPKRDVWVYGVADQYAEQVGEVDNVTLTSMVK-----KVDYVEDV-TRKASDGK 291
QY 361 LAGFPGKSAIVYIGIDRPVADIADTSLBGNDKLALEAISAKKEP-----FEK 411
Db 292 PFGGS-----TLTYGLDQDVGISPSKONLSDVY--KAVDKMKIINDGLEIPATEKE 343
QY 412 TKTIIPAE 418
Db 344 LKTFKAE 350

RESULT 8

H71340
membrane lipoprotein TmpC precursor - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 07-Aug-1998 #sequence_revision 07-Aug-1998 #text_change 09-Jul-2004
C:Accession: H71340; A43595; S29561
R:Fraser, C.M.; Norris, S.J.; Weisslock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Ueterbach, T.; McDo
rthy, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A>Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9655876
A:Accession: H71340
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-353 <COL>
A:Cross-references: UNIPROT:P29724; GB:AE001211; GB:AE000520; NID:93322582; PIDN:AAC6530;
A:Experimental source: Strain Nichols
R:Schouls, L.M.; van der Heide, H.G.J.; van Embden, J.D.A.
Infect. Immun. 59, 3536-3546, 1991
A>Title: Characterization of the 35-kilodalton Treponema pallidum subsp. pallidum recomb
A:Reference number: A43595; MUID:91372962; PMID:1894360
A:Accession: A43595
A:Molecule type: DNA
A:Residues: 1-10, 'A', 12-158, 'R', 160-353 <SCH>
A:Cross-references: GB:X57836; NID:948838; PIDN:CAA40968.1; PID:9581809
A>Note: this protein is shown to incorporate palmitic acid
C:Genetics:
A:Gene: tmpC; TP0319
A:Start codon: GTG
C:Superfamily: ABC transporter yuFn
C:Keywords: blocked amino end; lipoprotein; membrane protein; thiolester bond
F:1-20/Domain: signal sequence #statue predicted <SIG>
F:21-353/Product: membrane lipoprotein tmpC #statue predicted <MAT>
F:21/Modified site: fatty acylated amino end (Cys) (in mature form)
F:21/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #statue predicted

Query Match 7.9%; Score 182; DB 1; Length 353;
Best Local Similarity 23.7%; Pred. No. 0.00077;
Matches 86; Conservative 69; Mismatches 134; Indels 74; Gaps 17;

QY 80 MAITTAGTVNNDNSFNQSSWEAIIQGLGALTGGEITSVDSST-ALEBKYSIANTNKNW 138
Db 42 VGMVTDSDGIDDKSFFNQVWEGISRFQENNAKCKYTTASIDAYVPSLSAFADENGLV 101
QY 139 VLSGFQHGDAFTRWLKIPENKQIFTEKNIIILGIDWTDTENVIPTRGYINLTYTEAGW 198
Db 102 VACGSFLVEA-----VIFTSARFPKQFLVIDAVVDNRDV-----VSAVFGQNGSF 149
QY 199 LAGYANASFLAKKPPSDPTKSAI-VIGG--GISPAVTFIAGYLAGIKAMLNKSDK 254
Db 150 LVGVA--AALKKE-----AKSAVGFIVGMELGMPPL--FEAGFEAGVKAVD----- 193
QY 255 TKITTDKRIEINLGFVDVT--STKERLEQIASK--DKPSTLLAVG-----PLTIFSDII 306
Db 194 -----PDIOVVEVANTFSDPKQGLAALAYDSGVNIVFOVAGGTGNGVIREADR 246
QY 307 ANQNDRYILGVDTQSH--VYTKTRNKFSTILKNLGYSVFSLDLYTKKSNRNLAGF 364
Db 247 LMGDVMVIGDRQQYMDGVYDGSKSVYLTSMVRA-----DVAABKISMAVYGSFPG- 300
QY 365 EFGKSAIVYIGIDRPVADIADTSLBGNDKLALEAISAKKEPTEKTIIPAEVKTLL 424
Db 301 -----GGSIMFGLEDKAVGPIE-----ENPNLSAIVMEKIRSPERKI-----VSKXI 342
QY 425 EIP 427
Db 343 VVP 345

RESULT 9

F72418

basic membrane protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: F72418

R:Neilsen, K.E.; Clayton, R.A.; Gill, S.R.; Gilm, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, G.; Garret, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: F72418

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-359 <ARN>

A:Cross-references: UNIPROT:Q9WKV7; GB:AE001696; GB:AE000512; NID:g4980582; PIDN:AA03518

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM0102

C:Superfamily: ABC transporter yuFN

Query Match 7.9%; Score 181.5; DB 2; Length 359;

Best Local Similarity 23.9%; Pred. No. 0.00084;

Matches 94; Conservative 60; Mismatches 176; Indels 63; Gaps 16;

QY 61 RKSEIMAKADANKHGLNMAIVTAGTVNDNSFNQSSWEAIOQLGALTGEITSVDS-S 119

DB 2 RKFLVILMLFAVALFGKVIWTVDGGLGDSFNDRGKQAEELGIEAVIGSYE 61

QY 120 TAELEGKYSILANTNKVWVLSGFQHGDAFTKMLKIPENKOLFTEKNIILIGIDWTDTE- 178

DB 62 QSDYIPMLSKAAEADLVFAVGFMNTNDLFFKAKQYPTD-----YFGIDITPEEG 112

QY 179 NVITPTGVINTYKTEEGWLAGYANASFLAKKPPSDPTKSAIVIGGIS-PAYTFEIA 237

DB 113 QILP--NVLTFTFEQEAFLVGYAAM-----TKGVMGFVGGIPIPEVRRY 161

QY 238 GYLGIKAMNKNDSKDKTKI-----TTDKIEINLGFVDVDTSTKRLDQI----- 282

DB 162 GYEGKITYSVLAK-KVAKILRGTYDPEPKKDLAMSPAGADLVFPAASGACGCV 220

QY 283 --ASKDKPSTLLAVAGPTEIFSDIINANDRYLIGVDTDSLVTYTKNKFSTILKNL 340

DB 221 IEAREKESA-LAGSDKLVLDIDYTTNGKGFPAIGVMDQVM---APGAVLTSAMRV 276

QY 341 GYSFVSLSLDYTKKSNRLAGFEFGKSAIVYLGIDKRFVDIADISLEGNDKLA TEA 400

DB 277 DVASYGVVWAVE-----GTFEGGR---VLGISDAVGI--SPMKYTKGLVPRNV 322

QY 401 ISE---AKKEFEKTKTIP-AEVRKTLPIEM 429

DB 323 IAEILLYLEKMKETLKVETQELDAFEVPOI 355

RESULT 10

E70147 basic membrane lipoprotein B (bmbp) - Lyme disease spirochete

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C:Accession: E70147; I40290; I40242

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Keriavaga, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943; PMID:9403685

A:Accession: E70147

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-341 <KLE>

A:Cross-references: UNIPROT:Q45011; GB:AE001143; GB:AE000783; NID:g2688279; PIDN:AA06675

A:Experimental source: strain B31

R:Simpson, W.J.; Cieplak, W.

FEMS Microbiol. Lett. 119, 381-389, 1994

A:Title: Nucleotide sequence and analysis of the gene in Borrelia burgdorferi encoding t

A:Reference number: 140289; MUID:94327086; PMID:8050720

A:Accession: I40290

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-232, 'A', 234-317, 'V', 319-341 <RES>

A:Cross-references: GB:I24194; NID:g508420; PIDN:AAA72407.1; PID:g508422

R:Ojaimi, C.; Davidson, B.E.; Saint Girons, I.; Old, I.G.

Microbiology 140, 2931-2940, 1994

A:Title: Conservation of gene arrangement and an unusual organization of rRNA genes in t

A:Reference number: 140241; MUID:95111614; PMID:7812434

A:Accession: I40242

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-44, 'A', 46-179 <RE2>

A:Cross-references: GB:I35050; NID:g516591; PIDN:AA041402.1; PID:g551744

A:Experimental source: basic membrane protein C

Query Match 7.7%; Score 178; DB 2; Length 341;

Best Local Similarity 26.7%; Pred. No. 0.0013;

Matches 100; Conservative 60; Mismatches 123; Indels 92; Gaps 25;

QY 72 ANKHFGLNMAIVTAGTVNDNSFNQSSWEAIOQLGALTGEITSVDSSTAELEGKYS-- 129

DB 24 SSKIKIKISMLV--DGLVDDKSFNSANBALRLKQFPENIEVFS--CAISGVSSYV 78

QY 130 --LANTKN-----VWVLSGFQHGDAFTKMLKIPENKOLFTEKNI--ILGIDWTDNTVI 181

DB 79 SDDLNLKRNQSDLIW-LVGMVLTDA--SLVSSSNPKI--SYGIDIDYGDQVQIPELNI 133

QY 182 PGRYINLTKTEBAGWLAGY--ANASFLAKKPPSDPTKSAIVIG--GGISPAVTD-FI 236

DB 134 A-----VVRVREGALAGIAAKKSFSGK-----IGTIGMKKGIIVDAFR 174

QY 237 AGYLAGIKAMNKNDSKDKTKITTDKIEINLGFVDVDTSTKRLDQIASK--DKPSTLLAV 294

DB 175 YGESGAKVAV-KDIEIIEVSNSFSDVDIG-----RTIASKMYSKIDIVIH 221

QY 295 AGPLTEL-FSDIYANQND-RYLIGVDTDOSLVYTKNKFSTILKNLGSVFSVLSLDY 352

DB 222 AAGLAGIGVETAKNLDBGYVIGADDDG--YLAAPN-FTTSYIKNIGALYLTGE-Y 277

QY 353 TKKSNRLAGFEFGKSAIVYLGIDKRFVDIADISLEGNDKLA TEAISEAKKEPEKT 412

DB 278 IKANNV-----WESGK--VYQMGRLDGVIGLPAN-----EF-EYI 310

QY 413 KITPAEVRKTLPI 427

DB 311 KVLERKTIINKEIIVP 325

RESULT 11

AH1610 CD4+ T cell-stimulating antigen, lipoprotein [imported] - Listeria innocua (strain Clp1)

C:Species: Listeria innocua

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AH1610

R:Glaser, P.; Fraigneul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Feihl, H. ; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kretz, U.; Kuhn, M.; Kunz, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schlutener, T.; Simoes, N.; Talariz, A.; Valquez-Boland, J.A.; Voser, H.; Wehland, A.; Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AH1610

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-357 <GLA>

A:Cross-references: UNIPROT:Q92BM7; GB:AL592022; PIDN:CAC96656.1; PID:g16413898; GSPDB:GN

A:Experimental source: strain Clp11262

C:Genetics:

A:Gene: tcea
C:Superfamily: ABC transporter ynfN

Query Match 7.6%; Score 174; DB 2; Length 357;
Best Local Similarity 24.2%; Pred. No. 0.0024;
Matches 101; Conservative 62; Mismatches 137; Indels 118; Gaps 23;

QY 55 SGLV-----NEKSEIMAKADANHGFLNMAIVTAGTVNDNSFNQSSWEALIQQLG 106
DB 16 SGVVLGACGSSDDKKS-----GDDKSKDPTVAMVTDGTGVDPRSFNQSAWEGIAQFQG 69
QY 107 ALT-----GGEITVSSTAELEGKYSILANTNKVWVLS-----GFGGDAFTRLX 154
DB 70 KANMEKGTGDIYVQSSEADYK-----TNLNTAVRSVDYDLIYIGYKLDALIEVSK 123
QY 155 -IPENKQFTEKNIIILIGDWTDTENVIPTRGYINLYKTEBAGWLAGYANASFLAKKP 213
DB 124 QKPNQFIVDDTI-----DNRNVYSIG-----FKNDGSLYGVAGL----- 163
QY 214 SDPTKSAIVIGGISPAVTD-FLAGLAGIKAMNLKNSDKKTKITTDKIEINIGFDVQ- 271
DB 164 --TTKTNKVGFGVGKAVIDRFEGAFYAGVKA-----VNPNAQIDVQY 205
QY 272 --DPTKRLKQIASKDKPS-----TLAVAGPLTEIFSDITANQNR-----YLIGVDT 319
DB 206 ANDPAKADKGGQIASSMYSSGVVIFHAAGGTGNGVFAL-AKNLKKQPSRAVWVIGYDR 264
QY 320 DQ-----SLVYTKNKPFSTILKNLGYSVFVSLDYTKKNSRNLAG-FEFGKKSAT 372
DB 265 DQMBGKTYANDGADYNTLTSEIKRVIAV---DDLAT-----RTAAGFPFGTK--- 312
QY 373 YLIGKQRFVDIADTSLGNDKLTATEAISAKKEFEKTKTTPAEVRYKLTLEIPMP 430
DB 313 IEYGLDKAVGLSE-----HODNISKDVLAKE---EYKQKIVDGD-----IKVPEKP 357

RESULT 12

H70147
basic membrane protein D (bmpd) homolog - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999
C:Accession: H70147
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Latchura, R.; White
son, D.; Peterson, J.; Kervilange, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: H70147
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-360 <KLE>
A:Cross-references: GB:AE001144; GB:AE000783; NID:g2688291; PIDN:AA891505.1; PID:g268829
A:Experimental source: Strain B31
C:Superfamily: basic membrane protein C

Query Match 7.4%; Score 169.5; DB 2; Length 360;
Best Local Similarity 25.4%; Pred. No. 0.0045;
Matches 88; Conservative 64; Mismatches 137; Indels 57; Gaps 20;

QY 65 IMAAKADANKHFGLNMAIVTAGTVNDNSFNQSSWEALIQQLGALTGGEITVSSTAELE 124
DB 34 VACSSSDGKSEAKTVSLI-VDGAFFDDKGFNNESSKAIKRLKADLNINIEKASTGNSYL 92
QY 125 KXSSSLANTNGK-WVLSGFQHGDAFTMLKIPENKQFTEKNIIILIGDWTDTENVIP 183
DB 93 GDINLLEGNLTMGI-GFRLSDIL--FORASEVAVS---NVAI--IEGVYEIOIPLK 143
QY 184 GRVYNLYKTEBAGWLAGYANASFLAKKPSDPTKSAIVIGGISPAVTD-FLAGYLAG 242
DB 144 -NLNLSRSEBVAFLAGY-----PASKASTGTGIGVGVGKGLVLESFMIGYBAG 193

QY 243 IKAMNLKNSDKTKYITDKI-----EINLGFVDQDSTKRELBQIASDKPSTLLAVAGPL 298
DB 194 AKYAN-----SNIKVYSQYVTFGDFGLG-----RSTASNM---YBDGVDIIFPAAG-L 238
QY 299 TEIFSDIIANO-NDRLIGVDVDSLVYRTKKNKFTSILKNLGYSVFVSLDYTLTKRS 356
DB 239 SGIGVITNAKELGPDHYIIGVDQDQSYL---APNNVYSAVKKVDLSLMTSL-----TKKY 290
QY 357 NSRNIAFEFGKKSATVYLGK-DRFVDIADTSLGNDKLTATEAI 401
DB 291 LETGV--LDGSK---TWFLGKEDGLVLVNNLNKNSYSEIYNKSL 331

RESULT 13

AD1248
CD4+ T cell-stimulating antigen, lipoprotein [imported] - Listeria monocytogenes (strain
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AD1248
R:Glaser, P.; Franke, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entlian, K.D.; Fahl, H.,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, U.; Kuhn, M.; Kunz, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1248
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <GLA>
A:Cross-references: UNIPROT:Q48754; GB:NC_003210; PIDN:CAC9466.1; PID:G16410817; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: tcea
C:Superfamily: ABC transporter ynfN

Query Match 7.4%; Score 169; DB 2; Length 357;
Best Local Similarity 23.8%; Pred. No. 0.0048;
Matches 98; Conservative 63; Mismatches 144; Indels 106; Gaps 22;

QY 54 ISGLVNRKSEIMAKADANKHFGLNMAIVTAGTVNDNSFNQSSWEALIQQLGALT----- 109
DB 19 ILGCGSSDDKSKSDKSDKDF--TVAMVTDGTGVDPRSFNQSAWEGIAQFQANDMEK 76
QY 110 GGEITVSSTAELEGKYSILANTNKVWVLS-----GFGGDAFTRLX-IPENKQ 160
DB 77 GTDGYNTLQASSEADYK-----TNLNTAVRSVDYLYGIGYKLDALIEBVSXKQKPNQF 130
QY 161 LPTKKNIIILIGDWTDTENVIPTRGYINLYKTEBAGWLAGYANASFLAKKPSDPTKRS 220
DB 131 AIVDDTI-----DNRNVYSIG-----FKNDGSLYGVAGL-----TTKTN 168
QY 221 AIVGGISPAYVD-FLAGLAGIKAMNLKNSDKKTKITTDKIEINIGFDVQ---DPTK 276
DB 169 KVGFGVGKGTVIDRFEGAFYAGVKA-----VNPNAQIDVQYANDPAKA 212
QY 277 ERLEQIASDKPS-----TLAVAGPLTEIFSDITANQNR-----YLIGVDTQ----- 321
DB 213 DKGGIASSMYSSGVVIFHAAGGTGNGVFAL-AKNLKKQPSRAVWVIGVDRQWMEBK 271
QY 322 -SLVYTKNKPFSTILKNLGYSVFVSLDYTKKNSRNLAG-FEFGKKSATVYLGKID 379
DB 272 VTANDGADYNTLTSEIKRVIAV---DDLAT-----RAKAGDFPFGTK---IEYGLDK 319
QY 380 RFDVIADTSLGNDKLTATEAISAKKEFEKTKTTPAEVRYKLTLEIPMP 430
DB 320 DAVGLSE-----HODNISKDVLAKE---EYKQKIVDGD-----IKVPEKP 357

RESULT 14

C82914
conserved hypothetical membrane lipoprotein U0226 [imported] - Ureaplasma urealyticum

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2004, 01:14:44 ; Search time 127.457 Seconds
(without alignments)
2035.941 Million cell updates/sec

Title: US-09-676-249D-2
Perfect score: 2299
Sequence: 1 MKKKIKMKRFLGLVFLPLS.....KPPDKQOESLKLITDINKN 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_02.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	706	30.7	457	2	Q48902 mycoplasma
2	554.5	24.1	461	2	Q980L5 mycoplasma
3	467.5	20.3	491	2	Q6K1Q4 mycoplasma
4	467.5	20.3	491	2	AAT27522 mycoplasma
5	438.5	19.1	468	2	Q6E5B5 mycoplasma
6	417	18.1	465	2	Q9X775 mycoplasma
7	400.5	17.4	428	2	Q52311 mycoplasma
8	397.5	17.3	428	2	Q9RGX5 mycoplasma
9	394.5	17.2	428	2	Q32417 mycoplasma
10	394	17.1	428	2	Q9RGX4 mycoplasma
11	394	17.1	428	2	Q9RGX6 mycoplasma
12	393.5	17.1	428	2	Q9RGX7 mycoplasma
13	389.5	16.9	428	2	Q9RGX3 mycoplasma
14	387.5	16.9	428	2	Q9R3N6 mycoplasma
15	247	10.7	352	2	Q6RCY2 mycoplasma
16	238	10.4	457	2	Q6F0E8 mesoplasma
17	232.5	10.1	350	2	Q992H4 mycoplasma
18	229.5	10.0	349	2	Q9EV91 clostridium
19	227.5	9.9	349	2	Q878P8 streptococc
20	226.5	9.9	349	2	Q8DUJ6 streptococc
21	226.5	9.9	349	2	Q8K7C9 streptococc
22	224.5	9.8	350	2	Q8F0W2 streptococc
23	223	9.7	350	2	Q97RH0 streptococc
24	219	9.5	374	2	Q8DQC2 streptococc
25	215.5	9.4	349	2	Q8E5N9 streptococc
26	215.5	9.4	349	2	Q8E5N9 streptococc
27	211	9.2	359	2	Q898S3 clostridium
28	210	9.1	361	2	Q81A05 bacillus ce
29	207	9.0	350	2	Q9CFM9 mycoplasma
30	197	8.6	347	2	Q8E1F0 streptococc
31	197	8.6	347	2	Q8E6W8 streptococc

32	197	8.6	466	2	Q7WU11 spiroplasma
33	195.5	8.5	357	2	Q97L60 clostridium
34	194.5	8.5	550	2	Q6MUL7 mycoplasma
35	194.5	8.5	550	2	CAE76664 mycoplasma
36	191.5	8.3	347	2	Q79YMS streptococc
37	191.5	8.3	347	2	Q8K8S6 streptococc
38	190.5	8.3	357	2	Q83919 enterococcu
39	188	8.2	368	2	Q8FX05 bruceella su
40	187.5	8.2	347	2	Q8P2U0 streptococc
41	187.5	8.2	516	2	Q9PRD3 ureaplasma
42	185.5	8.1	350	1	YUEN BACSU bacillus su
43	185.5	8.1	355	2	Q732T4 bacillus ce
44	185.5	8.1	355	2	AA542731 bacillus
45	184	8.0	325	1	BMPA_BORGA borrelia ga

ALIGNMENTS

RESULT 1	Q48902	PRELIMINARY	PRT;	457 AA.
ID	Q48902			
AC	Q48902			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, last annotation update)			
DE	Ag 243-5 protein precursor.			
OS	Mycoplasma arginini.			
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.			
OX	NCBI_TaxID=2094;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96163149; PubMed=8551970;			
RA	Uehio S., Iwaki K., Tanai M., Ohta T., Fukuda S., Sugimura K.,			
RA	Kurimoco M.,			
RT	"Metabolic promoting activity of a novel molecule, Ag 243-5 derived from Mycoplasma and the determination of the complete nucleotide sequence."			
RL	Microbiol. Immunol. 39:393-400(1995).			
DR	EMBL, D16674; BAA04082.1; -			
DR	GO: GO:0008289; F: lipid binding; IEA.			
DR	InterPro; IPR003760; Bmp.			
DR	Pfam; PF02608; Bmp; 1.			
DR	PRINTS; PR01733; LIIPROTEIN48.			
KW	Signal.			
FT	SIGNAL 1 25 Potential.			
FT	CHAIN 26 457 Ag 243-5 protein.			
SQ	SEQUENCE 457 AA; 50789 MW; 9AEEBA11620CB22F CRC64;			
Query Match	30.7%; Score 706; DB 2; Length 457;			
Best Local Similarity	38.4%; Pred. No. 2.7e-35;			
Matches	173; Conservative 87; Mismatches 145; Indels 46; Gaps 16;			
QY	14 GLVFLPSAIAIT-ISAGCWDKETTKEKSDADNOKQITDVSKISGLVNERKSEIWAAYADA 72			
DB	12 GTISTVASVATFVSCG---ETDKKGLI-----RIDP-----NSFVDRQAEIKA----- 54			
QY	73 NKHFGMLAVTAGVGNVDSFNQSSWEAI-----QQLGALTG-GETTSVDSSTAELEGRY 127			
DB	55 -KNDFEFTVLTITAGGTVDKSPFNQSIWEAVLEHYDQIEKTTNLDPRVQETNNOSELIGKY 113			
QY	128 SSIANTKNNVWVLSFGPHGAFTRMKLIPEN-----KQLTEKNIIILIGDW---TTEEN 179			
DB	114 KNFLNGKNVWVLTITAGGTVDKSPFNQSIWEAVLEHYDQIEKTTNLDPRVQETNNOSELIGKY 173			
QY	180 VIPTGRYINLTYTEAGWLAGYANASFLAKKPPSPDPTKSAIVIGGISPVAVTDFIAGY 239			
DB	174 LKRGHRTISLXKTEBAGFIAGYASSKFLAYKFPNDAKRTIAPFGGHHGAVTDPIAGF 233			
QY	240 LAGIKANNLKNSSDKKITTDKTEINIGFDVQDTSTYERLEQJASKQSPSTLAAVAPLT 299			
DB	234 LAGIAKYNNDNPTAKVTISDNNINIDYGF-ISNDKTAFTINGVKNK--SLVLPVAGSLT 290			

QY 300 EIFSDII--ANQNDRIYLGVDTPDQSLVYTKTKNNKFTSILKNLGYSVFSVLSIDLYTKKN 357
D 291 SSVVDALIKSKNDKTYLIGVDTPDQSKIFSPA-TVFFTSIEKHGLSTIYQVLTIDMLKED 349
QY 358 SRNLAGEFGK----KSAIVYLGIKDRFVDADNLSLENDKKALTEALSEAKKEFEETK 413
D 350 SKFLGSPFSFLTPNPANATYKGISDDFVGVNSTVADADKVAQOEFLNEATDAFKQIQ 409
QY 414 TIPAEVRKTLIEPEM--PDKOPDKQESL 441
D 410 ANPT-NYKSVLGIPITMLINDADAKNEKSL 439

RESULT 2

Q980L5 PRELIMINARY; PRT; 461 AA.
ID 0980L5
AC 0980L5
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE ABC TRANSPORTER XYLOSE-BINDING LIPOPROTEIN.
GN OrderedLocustNames=MYPU_3460;
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP.
RX MEDLINE=21267165; PubMed=11353084;
RA Chmabud I., Helling R., Fietris S., Barbe V., Samson D., Gallsen P.,
Mozer I., Dybvig K., Wroblewski H., Viart A., Rocha E.P.C.,
Blanchard A.;
RA "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis";
RL Nucleic Acids Res. 29;2145-2153 (2001).
DR EMBL; AL445564; CAC13519.1; -.
DR PIR; B90555; B90555.
DR MYDULst; MYPU_3460; -.
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR003760; Bmp.
DR InterPro; IPR008107; Mycoplasma_p48.
DR InterPro; IPR011050; Pectin_lyas_like.
DR Pfam; PF02608; Bmp; 1.
DR PRINTS; PR01733; LIPOPROTEIN48.
KW Complete proteome; Lipoprotein.
SQ SEQUENCE 461 AA; 51096 MW; 6724D4D820809CE4 CRC64;

Query Match 24.1%; Score 554.5; DB 2; Length 461;
Best Local Similarity 30.3%; Pred. No. 6e-26;
Matches 140; Conservative 88; Mismatches 175; Indels 59; Gaps 13;
QY 5 IKMKKFLGLVPLPSAATISAGCWDKETKEKSNANONKOIT--DVSKISGLVNER- 61
D 1 MKLKK--KLFSITLVAAALALPATF-----VSCAQNPKNKINSNLDSSKITDLSQKE 51
QY 62 -----KSRIMAKADANHFGLNMAIVTAGGTVDNNSFNOSWEA1QQI GALTGGEI 113
D 52 VTEQKIYENKIKQASLETK-----VYLITADGNIDKSFNOQVYESQKTLKDFVDKAY 106
QY 114 TS-----VDSSTAELBKKYSSLANTKNVAVLSGFQHGDAFTRMKIPENK 159
D 107 KSQKKEAKENQKLDNINYSIAVKDLSEONKYKVALDRGYTTWILTFQOGGEIENFLDENNL 166
QY 160 QLFTEKNIIILIGIMWTDEN-VIPGRYINLTYTEEAGVLAGYANSAFLAKKFPSPDPTK 218
D 167 RRFENKKGKIIIGVAPNANSKITPQSGSLISLFTTEAGWQAGYASADFLGTKANNAK 226
QY 219 RSAIVTGGISPAVYDFIAGYIAGIKAWN--LKNSDKTKKITTTKIEINLGFVDOTSTK 276
D 227 RAISAFGGGAGVYDFLNGFFBGRAMNSSEAKNANKVKYVSENVLVDITGF-IPNAEK 285
QY 277 ERLQIASKDKPSTLLAVAGPLTEIFSDII--ANQNDRIYLGVDTPDQSLVYTKTKNKF 333

D 286 EVSNVNETGKSTISLPAAGFTGVVDVLRKDTSDERFIVGVDTPDQSLFNDSKRF 345
QY 334 TSILKNLGYSVFSVLSIDLYT-----KKSNSHLNLAFFEGKKSATVYLGIKDRFPVIA 385
D 346 TSIYKNIAFPVYQILALLRLKDESVYLKSGNDKFLGS---NPNKVLKKGSLAKFPVNT 402
QY 386 DTSLEGNDDKALTEALISEA--KKEFEETKTIPEAVRKTL 425
D 403 KSRVKEISIKTQADTSIQKIDKMANPNNSKKIEKEMTNCBLE 444

RESULT 3

Q6KIQ4 PRELIMINARY; PRT; 491 AA.
ID Q6KIQ4
AC Q6KIQ4
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Unspecified sugar ABC transporter binding protein.
GN OrderedLocustNames=WMOB0360;
OS Mycoplasma mobile.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=163K / ATCC 43663;
RA Birren B.W., Strange-Thomann N., Smith C., Decaprio D., Fisher S.,
Butler J., Galvo S., Elkin T., Fitzgerald M.G., Hafer N., Kodira C.D.,
Major J., Wang S., Wilkinson J., Nicol R., Nusbbaum C.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR InterPro; IPR008107; Mycoplasma_p48.
DR PRINTS; PR01733; LIPOPROTEIN48.
KW Complete proteome.
SQ SEQUENCE 491 AA; 52817 MW; 2D1C707687771B41 CRC64;

Query Match 20.3%; Score 467.5; DB 2; Length 491;
Best Local Similarity 29.7%; Pred. No. 1.5e-20;
Matches 141; Conservative 80; Mismatches 165; Indels 89; Gaps 18;
QY 43 NQNKQITDVSKISGLVNERKSEIIMAAKADANKHGLNMAIVTAGGTVDNNSFNOSWEA1 102
D 32 NTGLRVTDNOVFRDLVASREAFATQRVANNLSJNSKTLTLLTAGGVNDSPNOSINEAL 91
QY 103 QQLGALTG--GEITSVVSSTA---ELEBKYSILANTKNVAVLSGFQHGDAFTRMKIP 157
D 92 LEIRQTKGKGNBSFATTTAGTPQLQRYDQALFFNHKFWVLTFQODGAFQWLDIGN 151
QY 158 NKQLFTEKNIIILIGIMWTDENVIPGRYINLTYTEEAGVLAGYANSAFLAKKFPSPDPT 217
D 152 NRAEFIRKQYIIVADWTMLLEVPQGFISINVRTOSSWIVGNAAKFIIDNHNN-- 209
QY 218 KRSIVTGGISPAVYDFIAGYIAGIKAWNLS-----DKTKKITP-DKIEI 264
D 210 -RTFNTFGGAFPPVIVNFNAGFLGILDEN--NSTFLPEBETSTITDKKSLFTPGDINI 266
QY 265 NLGFVDOTSTKERLEQIASKDKPST--LLAVAGPLTEIFSDIIANQND-RYLIGVDTQ 321
D 267 NTGPAV---TPBAATLIQSIIVSGTGQVFPVAGSLTLLIVNLSIQNSQGFVIGVDSQ 322
QY 322 SLVYTKTKN--FETSILKNLGYSVFSVLSIDLY-----TKKNS 358
D 323 AKAFSPDLAKLFFSVEKNAVAGTYVALASLYIGTAVTDPEFNITGSSRFIPYTERKNS 382
QY 359 RNLAGFEFGKSAIVYIGIDR-----FVDIADTSLEGNDDKALTEA-----ISEAK 408
D 383 SSIP-----LANADITGFVFESETPVDVFGSKALGGKTTQSLVQNVGSGSFAVDEY 437
QY 409 -----BEKTK---TIPAEVRKTLIEPEM--DKOPDKQESLKITDIN 449
D 438 LAASLALFNKAKKIITIP-----VQLPNPSGGGSTPEQIPLNELIKIN 485

RESULT 4
AAT27522 PRELIMINARY; PRT; 491 AA.
AC AAT27522;
DT 24-MAY-2004 (TREMBlrel. 27, Created)
DT 24-MAY-2004 (TREMBlrel. 27, Last sequence update)
DE Unspecified sugar ABC transporter binding protein.
GN MYO0360.
OS Mycoplasma mobile 163K.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma;
OC Mycoplasma mobile.
OX NCBI_TaxID=267748;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=163K;
RA Berg H.C.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=163K;
RA Birren B.W., Stange-Thomann N., Smith C., Decaprio D., Fisher S.,
RA Butler J., Calvo S., Ekin T., Fitzgerald M.G., Hafez N., Kodira C.D.,
RA Major J., Wang S., Wilkinson J., Nicol R., Nuebaum C.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=163K;
RA Jaffe J.D., Church G.M.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AEO17337; AAT27522.1; -
SQ SEQUENCE 491 AA; 52817 MW; 2D1C70768771B41 CRC64;

Query Match 20.3%; Score 467.5; DB 2; Length 491;
Best Local Similarity 29.7%; Pred. No. 1.5e-20;
Matches 141; Conservative 80; Mismatches 165; Indels 89; Gaps 18;

QY 43 NONKQITVSKISGLVNERSEIEMAAKADKNGHGLMAIVTAGTNDNSFNQSSWEAI 102
DB 32 NTGLRVTDNOVFRDLVASREAEFATQRVANNSLPNSKTLTLTAGGVNDLSFNQSSWEAI 91
QY 103 QOLGALTG--GEITSVDSSTA---ELEKYSILANTKNVNVLSGFQHGDAFTWKLPIE 157
DB 92 LEIGROTKRGKNSFAETTAGTPOQLQRODQALFFHHKFTVLTGFQDGAFOWLQIGN 151
QY 158 NKOLFTEKNIIIGIDMTDENVIPTGRYINLYKTEBAGMLAGYANASFLAKKPPSDPT 217
DB 152 NRAEFIRKQVIVADWTMLVLPPOQFISINRTQSSWIVGNAVAKFTSDNHNHN-- 209
QY 218 KBAIVIGGDISPVPDPIAGYLAGIKAMLNKS-----DKTKITL-DKIEI 264
DB 210 -RTFNTFGGAFPEVTNFGNFGLOGILDFN--NSTLEPGFTSTTDKKLSFTGDIINI 266
QY 265 NLGFDVQDTSTKERLEQIASKDKPST--LLAVAGPLTEIFSDIIANQND--RYLIGVDTQ 321
DB 267 NTGFAV---TPEAKATIGSVSGTQVFPVAGSLTLTLTANSLQSGNSGQFVIGVDSQ 322
QY 322 SLVYTKTKNK-FTSILKNLGYSVFVLSLY-----TKKNS 358
DB 323 AKAFSPDLAKLFFSSVEKNVAGTYALASLYLGTGSTDPDFNITGSSSRPIPTKKNNS 382
QY 359 RNLAGPFGKKSALVYVIGIKDR-----FVADIATSLGNDKDLATEA-----ISEAKKEP 408
DB 383 SSLP-----LANADITGVFESTEPVDFVGSFSGALGKTKTQSLVQANVGRSPFAVDEY 437
QY 409 -----BEKTK---TIPAEVRAKTLSEIPEMP--DKQPDKQOESDKLITDIN 449
DB 438 LAASLALFNKNKAKIATIP-----VQIFNFGSGSTPQGINPLNELIKKIN 485

RESULT 6
Q9X775 PRELIMINARY; PRT; 465 AA.
AC Q9X775;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE P48 membrane lipoprotein precursor.
GN Name=P48;
OS Mycoplasma agalactiae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20002620; PubMed=10531294;

QY 3 KXIKMKFGLGLVFPPLSATISAGCWDKETTKEKSAADNOKQITVSKISGLVNERK 62
DB 2 KKKKFFVFLGAA---PVLSPLVAASGCDKYFKETEVDG-----VKTVTLSHIYSRK 52
QY 63 SEIMAAKADANKHFGMLMAIVTAGTNDNSFNQSSWEAIQOLGALTGGEITSV----- 116
DB 53 LKLRDGLTVDN---APRAAFITDEGSVHDESFNQSWEAVHKISYELGLDKAQSNGKNL 109
QY 117 -----DSSTAELEKYSILANTKNVNVLSGFQHGDAFTWKLPIENKQOLFTEKNIIIG 171
DB 110 RNKRYEPEKKGELASSYKNAIDSSFRYVILCGFTHKAL--YGLPEYIKIKIKNNIVFIT 167
QY 172 IDMTDTENV-----IPTGRYINLYKTEBAGMLAGYANASFLAKKPPSDPTK 218
DB 168 VDDPIQDDASTGEPAAKAFYDKIGQGLVIVITDTPKAAVYIAGALADYRSKIYKDPK 227
QY 219 RSAIVIGGDISPVPDPIAGYLAGIKAMLNKSDKTKITTDKIEINLGFVDOTSTKER 278
DB 228 RTGAFGIGIPWPSVDPIAGTPOQIIDWNKEHEAKTKSLNNTIELTSF---TSGEFVA 284
QY 279 LEQIASKDKPSTLLAVAGPLTEIFSDIIANQND--RYLIGVDTQSLVYTKKN-----K 331
DB 285 VAAINSVYKATASYPVAGSLSPTAKEIKKLGKKNKFIIGVADQ-----KVALKGRH 337
QY 332 FPTSILKNLGYSVFVLSLYTKKNSRN--AGEFGKKS-----ATVYGIK 378
DB 338 IFTSVMKLIGQAVYNVLADYLSQGENSLSLQPGFELGKNGGEAKVFGYGENESKIVGVA 397
QY 379 DRFVDIADTS--LEGNDKILATPAISEAKKEFEKTKTIPAEVRAKTL--EIPF---MP 430
DB 398 -----TSGLDKSDKDEIANKALBEATKYISK-----KAEIKTLISQGLEAKKALG 444
QY 431 DKQPDKQOESLKLITDINK 450
DB 445 TKWPDQPADQFGKMINWLAK 464

RA Rosati S., Pozzi S., Robino P., Montinaro B., Conti A., Fadda M.,
RA Pletau M.;
RT "P48 major surface antigen of Mycoplasma agalactiae is homolog to a
RT major product of Mycoplasma fermentans and belongs to a selected family
RT of bacterial lipoproteins";
RL Infect. Immun. 67:6213-6216(1999).
DR EMBL; AJ132423; CAB43718.1;-.
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR003760; Bmp.
DR Pfam; PF02608; Bmp; 1.
DR PRINTS; PR01733; LIPOPROTEIN48.
DR Lipoprotein; Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 465 AA; 51149 MW; 60AD5448CFE03C96 CRC64;

Query Match 18.1%; Score 417; DB 2; Length 465;
Best Local Similarity 28.4%; Pred. No. 1.8e-17;
Matches 141; Conservative 94; Mismatches 180; Indels 82; Gaps 22;

QY 3 KKIKNNKFLGLVPLSAIATISAGCWDKETEKEKSNADNQNKOITDVSKISGL-VVER 61
DB 2 KKNKPYFLGMA---PVLSPVLVAASGDKYFKETEVDCVKTITSLAHITSRKGLKREG 58
QY 62 KSEIMAAKADANKHFGMLMAIVTAGTVNDNSFNQSSWEALIQGLALTGGEITVSSTA 121
DB 59 LTVENAPRA-----TFITDEGSVHDESFNQSGWEAVHAKVSYELGLDKAQV-SGNK 107
QY 122 ELEBK-----YSSLANTNNKNNVWLSGFOHGAFTRMKLIPEKNK-QLFTEKNII 168
DB 108 NLNNKVEPEPKGQLLEAKNAIDSGFRYIVLGFHQASL---VGLDENYIKKIKDNNII 164
QY 169 ILGIDWT---DTENV-----IPGRYINLYKTEBAGMLAGYANASFLAKFPPSDPTK 218
DB 165 FITVDPNLFTEDDANVKTFFIKKIGSHLVPIPTKQAAIYAGALADYFSQYVKDQEK 224
QY 219 RSAIVTGGGSPAVTDFIAGLAGIKANWLNKSDKTKITTDKIEINLGFVQDTSTKER 278
DB 225 RTIAGFGGIPMPAVSDFIAGTFQGIIDNNKEHPEAKTKSLNETIELNTLF---TSGTPQA 281
QY 279 LEQIASKQSPSTLAVAGPL-TEIFSDI--TANQDRFLIGVDQSLVYTKTKN----- 330
DB 282 TTAINSVVKAATASYPVAGSLSTIDRAKEIKLADK-DKTIIVDADQ-----KNALKGH 333
QY 331 KFTPTSLKNLGYSVSVLSDLYTKKNSRNL-AGFEFGKKSAT-VYLGIDK----RFYDI 384
DB 334 RIFTSVMKLIGQAVYNILADLYSKGENQLDLPQFEIGKKGKGTPTVFGYDTEDKQYGV 393
QY 385 ADTG-LEGNDKKLATETAISEAKKEFEKTKTTPAEVAKTLEI-----DPMDDKQ 433
DB 394 ATSGLLDDKNDKDEINKALKDATAYVVK-KT-----EIQSKDKDMETAKKALGAKFSDP 448
QY 434 PDKQESLDKLITDINK 450
DB 449 GGFQKQVMDWLASETRK 465

RESULT 7
052311
ID 052311 PRELIMINARY; PRT; 428 AA.
AC 052311;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Membrane lipoprotein P48v.
OS Mycoplasma fermentans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2115;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG18;
RA Rawadi G., Dyer K., Dujancourt A.;

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF036106; AAB99740.1;-.
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR003760; Bmp.
DR InterPro; IPR008107; Mycoplasma_p48.
DR Pfam; PF02608; Bmp; 1.
DR PRINTS; PR01733; LIPOPROTEIN48.
DR Lipoprotein.
SQ SEQUENCE 428 AA; 47862 MW; D9506E817E330EAA CRC64;

Query Match 17.4%; Score 400.5; DB 2; Length 428;
Best Local Similarity 27.3%; Pred. No. 1.7e-16;
Matches 129; Conservative 95; Mismatches 175; Indels 73; Gaps 21;

QY 5 IKNNKFLGLVPLSAI-ATISAGCWDKETEKEKSNADNQNKOI--TDVSKISGLVNER 61
DB 1 MKSKALLDGL-SPIALILPAVAVSC-----KNNDSNISFKRKDISKYTTTANG 50
QY 62 KSEIMAAKADANKHFGMLMAIVTAGTVNDNSFNQSSWEALIQGLALTGGEITVSSTA 121
DB 51 KQVKNAL-----LKKIPVILITDEGKIDKSFQSAFEALKAINKQITGEINSEPS-S 104
QY 122 ELEBGSLSANTNNKNNVWLSGFOHGAFTRMKLIPEKNKOLFTEKNIIILGIDWTENV 181
DB 105 NFESAINSALSAGKIVLVNLFKQOSIKQY--IDAREBLERQIKIGIDF-DITREY 161
QY 182 PTGRYINLYKTEBAGMLAGYANASFLAKFPPSDPTKRSALIVTGGISPATDFIAGYLA 241
DB 162 KW-FYSLQFNKISAFITGVALIASWLSQ---DESKRVVASFCGAFPGVTTNKGFAK 216
QY 242 GIKAMNLKNSDKTKIT-TDKIEINLGFVDQDTSTKERLQIAS-----KDKPST 290
DB 217 GILYNNQKH--KSYKFTHTSPVKLDSGF-----TAGKKNVTVINNVLSPPADVKYNPV 269
QY 291 ILAVAGPLTEIFSDIINQDRFLIGVDQSLVYTKKNNKFTSLKNLGYSVSVLSD 350
DB 270 ILSVAGPAT--FEVYKLANQGQYIVIGVSDQGM--QDKRILTSVLKHKQAYETLLD 325
QY 351 L-----YTKKNSRNLAGEFGKKSATVYLGIDKRPVVDIADTSLGNDKKL-ATE 399
DB 326 LIEKEGKYPYVVKDKKADKMSHFQTQ-----KEKIGVAENHFSNTEQAKINN 377
QY 400 AISEAKKEFEKTKTTPAEVAKTLEIPEMPD-KQPKQESLDKLITDINK 450
DB 378 KIKKAIKMFKE---LPEDFVKYINSDKALDKGNKIDNVSERLAIIISAIK 425

RESULT 8
09RGX5
ID 09RGX5 PRELIMINARY; PRT; 428 AA.
AC 09RGX5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Macrophage activating lipoprotein-404 precursor.
GN Name=malp;
OS Mycoplasma fermentans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2115;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SK5;
RX MEDLINE=99115554; PubMed=9916088;
RA Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
RT "Differential posttranslational processing confers intraspecies
RT variation of a major surface lipoprotein and a macrophage-activating
RT lipopeptide of Mycoplasma fermentans";
RL Infect. Immun. 67:760-771(1999).
DR EMBL; AF099211; AADI6395.1;-.
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR003760; Bmp.
DR InterPro; IPR008107; Mycoplasma_p48.
DR Pfam; PF02608; Bmp; 1.

DR PRINTS; PRO1733; LIPPROTEIN48.
 KM Lipoprotein; Signal.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 428 Macrophage activating lipoprotein-404.
 SQ SEQUENCE 428 AA; 47835 MW; D03F0F47EA2B1460 CRC64;
 Query Match 17.3%; Score 397.5; DB 2; Length 428;
 Best Local Similarity 27.0%; Pred. No. 2.6e-16;
 Matches 127; Conservative 100; Mismatches 174; Indels 69; Gaps 20;
 QY 5 IKNNKFLGLVPLSLAI-ATISAGCDKETTKEEKADONKOITVSKISGLVNERKS 63
 DB 1 MKSKSKILLGL-SPHAILPAVAVSCGNDES-----NISFKEXDISKTYTTNANGKQ 52
 QY 64 EIMAAKADAKHGHGMAIYTAGTVDNSFNOSWEAIOGLALTGELITSVDSSTAE 123
 DB 53 VKNAAEL-----LKLKPVLTIDEGKIDKSFNOSAFALAKINKQIGIEINVSPPS-SNF 106
 QY 124 EGRYSLANTNKNVWVLSGFQHDPAFTWLIKIPENKOLFTEKNIIIGIDTDTENVIPT 183
 DB 107 ESNVNSALSGHKIKWLVNGFKHQOSIKQY--IDAHRELEBNQIKIGIDF-DIETEKW 163
 QY 184 GRYINLTYTEBAGWLAGYANASFLAKPPSDPTKSAIYIGGISPAVDFLAGYLAGI 243
 DB 164 --FYSLOFNIKESAFITGVAIASWLSQ--DESKRVASFGGAPGVITFNEGFAKGI 218
 QY 244 KANNLKSDDKTKI-TTDKIEINLGFVDPTSTKERLEQIAS-----KDKPSTLL 292
 DB 219 LYNNQKH--KSKTYHTSPVKLDSGF-----TAGEKNATYINNVLSSTPADVKYNPVIL 271
 QY 293 AVAGPLTEIFSDIINANDRYLIGVDTQSLVYTKTKKFFTSILKNLGYSVESVLSDL- 351
 DB 272 SVAGPAP--FEYTRLANKGQYIVGSDQGM--QDDRLITSLVKIKQAVETLLDLI 327
 QY 352 -----YTKSNSRNLAGFEFGKKSATVYIGIKDPVDIADTSLGNDKDL-ATEAI 401
 DB 328 LEKEEGYKPYVVDKKADKKMSHGTO-----KEKWIGVABNHPSNTEBQAKINKKI 379
 QY 402 SEAKKEFEKTKTIPAEVVKLTLEIPMPD-KQPDKQGESLKITITINK 450
 DB 380 KEAIKMFKE---LPEDFVKYINSDKALKQGNKIDNVSERLEAITSAINK 425
 RESULT 9
 ID 032417 PRELIMINARY; PRT; 428 AA.
 AC 032417;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE M61AG.
 OS Mycoplasma fermentans.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2115;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=98022661; PubMed=9359703;
 RA Matsuno M., Takeda J., Inoue N., Hara T., Hatanaka M., Takahashi K.,
 RA Nagaawa S., Akedo H., Seya T.;
 RT "A novel protein that participates in nonself discrimination of
 RT malignant cells by homologous complement.";
 RL Nat. Med. 3:1266-1270(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98241611; PubMed=9575196;
 RA Matsuno M., Nishiguchi M., Kikawa S., Nishimura H., Nagaawa S.,
 RA Seya T.;
 RT "Structural and functional properties of complement-activating protein
 RT M61AG, a Mycoplasma fermentans gene product that induces cytokine
 RT production by human monocytes.";
 RL J. Biol. Chem. 273:12407-12414(1998).
 RN [3]

RP SEQUENCE FROM N.A.
 RA Seya T., Matsuno M.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D64083; BA23530.1;
 DR EMBL; AB026157; BA177211.2;
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR InterPro; IPR003760; Bmp.
 DR InterPro; IPR008107; Mycoplasma_p48.
 DR Pfam; PF02608; Bmp; 1.
 DR PRINTS; PRO1733; LIPPROTEIN48.
 SQ SEQUENCE 428 AA; 47862 MW; F43B078F21DAD06E CRC64;
 Query Match 17.2%; Score 394.5; DB 2; Length 428;
 Best Local Similarity 26.8%; Pred. No. 3.9e-16;
 Matches 126; Conservative 101; Mismatches 174; Indels 69; Gaps 20;
 QY 5 IKNNKFLGLVPLSLAI-ATISAGCDKETTKEEKADONKOITVSKISGLVNERKS 63
 DB 1 MKSKSKILLGL-SPHAILPAVAVSCGNDES-----NISFKEXDISKTYTTNANGKQ 52
 QY 64 EIMAAKADAKHGHGMAIYTAGTVDNSFNOSWEAIOGLALTGELITSVDSSTAE 123
 DB 53 VKNAAEL-----LKLKPVLTIDEGKIDKSFNOSAFALAKINKQIGIEINVSPPS-SNF 106
 QY 124 EGRYSLANTNKNVWVLSGFQHDPAFTWLIKIPENKOLFTEKNIIIGIDTDTENVIPT 183
 DB 107 ESNVNSALSGHKIKWLVNGFKHQOSIKQY--IDAHRELEBNQIKIGIDF-DIETEKW 163
 QY 184 GRYINLTYTEBAGWLAGYANASFLAKPPSDPTKSAIYIGGISPAVDFLAGYLAGI 243
 DB 164 --FYSLOFNIKESAFITGVAIASWLSQ--DESKRVASFGGAPGVITFNEGFAKGI 218
 QY 244 KANNLKSDDKTKI-TTDKIEINLGFVDPTSTKERLEQIAS-----KDKPSTLL 292
 DB 219 LYNNQKH--KSKTYHTSPVKLDSGF-----TAGEKNATYINNVLSSTPADVKYNPVIL 271
 QY 293 AVAGPLTEIFSDIINANDRYLIGVDTQSLVYTKTKKFFTSILKNLGYSVESVLSDL- 351
 DB 272 SVAGPAP--FEYTRLANKGQYIVGSDQGM--QDDRLITSLVKIKQAVETLLDLI 327
 QY 352 -----YTKSNSRNLAGFEFGKKSATVYIGIKDPVDIADTSLGNDKDL-ATEAI 401
 DB 328 LEKEEGYKPYVVDKKADKKMSHGTO-----KEKWIGVABNHPSNTEBQAKINKKI 379
 QY 402 SEAKKEFEKTKTIPAEVVKLTLEIPMPD-KQPDKQGESLKITITINK 450
 DB 380 KEAIKMFKE---LPEDFVKYINSDKALKQGNKIDNVSERLEAITSAINK 425
 RESULT 10
 ID 09RGX4 PRELIMINARY; PRT; 429 AA.
 AC 09RGX4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Macrophage activating lipoprotein-404 precursor.
 OS Name=malp; fermentans.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2115;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MT-2;
 RX MEDLINE=99115554; PubMed=9916088;
 RA Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
 RT "Differential posttranslational processing confers intraspecies
 RT variation of a major surface lipoprotein and a macrophage-activating
 RT lipopeptide of Mycoplasma fermentans.";
 RL Interf. Immun. 67:760-771(1999).
 DR EMBL; AF099212; AADI6396.1;
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR InterPro; IPR003760; Bmp.

DR InterPro; IPR008107; Mycoplasma_p48.
DR Pfam; PF02608; Bmp; 1.
DR PRINTS; PRO1733; LIPPROTEIN48.
KW Lipoprotein; Signal.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 429 macrophage activating lipoprotein-404.
SQ SEQUENCE 429 AA; 47933 MW; B6D08CF975AC3171 CRC64;
Query Match 17.1%; Score 394; DB 2; Length 429;
Best Local Similarity 27.0%; Pred. No. 4.2e-16;
Matches 127; Conservative 102; Mismatches 172; Indels 70; Gaps 21;
QY 5 IKNNKFLGLGVPLPSAI-ATISAGCWDKETTKEKSAADNQNKOITDVSKISGLVNERKS 63
DB 1 MKSKSKILLGL-SPIAAILPAVAVSCGNNDSE-----NISFKKDIISKYTTTNANQKQ 52
QY 64 EIMAKADANKHFGINNAIYTAGTVNDNSFNQSWEAIOQLALTGGEITSVDSSTAE 123
DB 53 VVKNAEL-----LTKLPVLTIDEGKIDKSPNQSAPFALKAINKQGTGEINNVPS-SNF 106
QY 124 EGYTSSLANTKNVWVLSGFQHGDAFTRMKIPENKQLFTEKNIIIGIDWTDTEENVIPT 183
DB 107 ESAVNSALSGHKIWLNGRFGHQSIKQY--IDAHRELEBNQIKIGIDF-DIETEKW 163
QY 184 GRYINLYTKEBAGWLAGYANASFLAKKFPSPDPTKSAIYIGGISPATDFIAGYLAGI 243
DB 164 --FYSLOFNIKESAFTTGVALASWLSQ---DESKRVASFGGAFPGVTFPNEGFAKGI 218
QY 244 KAMNLKNSDKTKI-TTDKIEINLGPVODSTYKERLEQIAS-----KDKPSTLL 292
DB 219 LYVQKH--KSKLYHTSPVKLDSGF-----TAGKKNVTIYNVLSTPADVKXNPVIL 271
QY 293 AVAGPLTEIFSDI-IANQNDRYLIGVDTQSLVYTKTKNKFETSLKNLGYSVFSVSDL 351
DB 272 SVAGPAT--PEYVALANKQGYIVGVDSDQGM--QDKDRLISVLGHITKQAVVETLLDL 327
QY 352 -----YTKSNSRNLAGFEFGKSAIVYLGIKORFVDIADTSLGNDKKL-ATEA 400
DB 328 ILKEEGYKPYVVDKADKWSHFQTQ-----KEKWIQVAENHFSNTEEQAKINNK 379
QY 401 ISEAKKEFEETKTITPAEVRKTLIEPMPD-KOPDQOESLDLITDINK 450
DB 380 IKEAIKMFKE---LPEDFVKYINSDKALKGNKLDIVSERLEAIIISAINK 426
RESULT 11
QYRGX6 PRELIMINARY; PRT; 429 AA.
AC QYRGX6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Macrophage activating lipoprotein-404 precursor.
GN Name=malp;
OS Mycoplasma fermentans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2115;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Incognitus;
RX MEDLINE=99115554; PubMed=9916088;
RA Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
RT "Differential posttranslational processing confers intraspecies
RT variation of a major surface lipoprotein and a macrophage-activating
RT lipopeptide of Mycoplasma fermentans.";
RL Infect. Immun. 67:760-771(1999).
DR EMBL; AF099210; AAD16394.1;-
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR003760; Bmp.
DR Pfam; PF02608; Bmp; 1.
DR PRINTS; PRO1733; LIPPROTEIN48.
KW Lipoprotein; Signal.

FT SIGNAL 1 24 Potential.
FT CHAIN 25 429 macrophage activating lipoprotein-404.
SQ SEQUENCE 429 AA; 47961 MW; B6D09A8812AC3171 CRC64;
Query Match 17.1%; Score 394; DB 2; Length 429;
Best Local Similarity 27.0%; Pred. No. 4.2e-16;
Matches 128; Conservative 101; Mismatches 169; Indels 76; Gaps 21;
QY 5 IKNNKFLGLGVPLPSAI-ATISAGCWDKETTKEKSAADNQNKOITDVSKISGLVNERKS 63
DB 1 MKSKSKILLGL-SPIAAILPAVAVSCGNNDSE-----NISFKKDIISKYTTTNANQKQ 52
QY 64 EIMAKADANKHFGINNAIYTAGTVNDNSFNQSWEAIOQLALTGGEITSVDSSTAE 123
DB 53 VVKNAEL-----LTKLPVLTIDEGKIDKSPNQSAPFALKAINKQGTGEINNVPS-SNF 106
QY 124 EGYTSSLANTKNVWVLSGFQHGDAFTRMKIPENKQLFTEKNIIIGIDWTDTEENVIPT 183
DB 107 ESAVNSALSGHKIWLNGRFGHQSIKQY--IDAHRELEBNQIKIGIDF-DIETEKW 163
QY 184 GRYINLYTKEBAGWLAGYANASFLAKKFPSPDPTKSAIYIGGISPATDFIAGYLAGI 243
DB 164 --FYSLOFNIKESAFTTGVALASWLSQ---DESKRVASFGGAFPGVTFPNEGFAKGI 218
QY 244 KAMNLKNSDKTKI-TTDKIEINLGPVODSTYKERLEQIAS-----KDKPSTLL 292
DB 219 LYVQKH--KSKLYHTSPVKLDSGF-----TAGKKNVTIYNVLSTPADVKXNPVIL 271
QY 293 AVAGPLTEIFSDI-IANQNDRYLIGVDTQSLVYTKTKNKFETSLKNLGYSVFSVSDL 351
DB 272 SVAGPAT--PEYVALANKQGYIVGVDSDQGM--QDKDRLISVLGHITKQAVVETLLDL 327
QY 352 -----YTKSNSRNLAGFEFGKSAIVYLGIKORFVDIADTSLGNDKKL-ATEA 400
DB 328 ILKEEGYKPYVVDKADKWSHFQTQ-----KEKWIQVAENHFSNTEEQAKINNK 379
QY 401 ISEAKKEF---EKTITTPAEVRKTLIEPMPD-KOPDQOESLDLITDINK 450
DB 380 IKEAIKMFKELPEDFVKYINSDKALKGNKLDIVSERLEAIIISAINK 426
RESULT 12
QYRGX7 PRELIMINARY; PRT; 428 AA.
AC QYRGX7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Macrophage activating lipoprotein-404 precursor.
GN Name=malp;
OS Mycoplasma fermentans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2115;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=II-29/1;
RX MEDLINE=99115554; PubMed=9916088;
RA Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
RT "Differential posttranslational processing confers intraspecies
RT variation of a major surface lipoprotein and a macrophage-activating
RT lipopeptide of Mycoplasma fermentans.";
RL Infect. Immun. 67:760-771(1999).
DR EMBL; AF099209; AAD16393.1;-
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR003760; Bmp.
DR Pfam; PF02608; Bmp; 1.
DR PRINTS; PRO1733; LIPPROTEIN48.
KW Lipoprotein; Signal.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 428 macrophage activating lipoprotein-404.
SQ SEQUENCE 428 AA; 47960 MW; D6B6C0BA965CFE1 CRC64;

Query Match 17.1%; Score 393.5; DB 2; Length 428;
 Best Local Similarity 26.8%; Pred. No. 4.5e-16;
 Matches 127; Conservative 97; Mismatches 178; Indels 71; Gaps 21;

QY 1 MKKKIKNNKFLGLVPLPSAI-ATISAGCWDKETEKEKSDADNQNKOITDVSKISGLVNERKS 60
 DB 1 MKKSKK--ILLGLSPIAAILPAAVAVSCG-----NNBESNISFKKXIKITTTN--ANE 50

QY 61 RKSEIMAAKADANKHFGNLMAIYTAGTVNDNSFNQSSWEAIQOLGALTGEITSDVSST 120
 DB 51 KQ--VVKNAELLK--LKPVLTIDEGKIDKSFNQSFAELKAIKQGTGIEINNVSPS- 103

QY 121 ALEEGKSSANTKNVWVLSGFQHGDAFTRWLKIPENKOLFTEKNIIILIGIMTWTENV 180
 DB 104 SNRESAYNSALSGHKIWLNGFRHQOSIKQY--IDARELERNOIKITIGID-DIETE 160

QY 181 IPTGRYINLTYTEEAGMLAGYANASFLAKKFPSPDKRSATVYIGIKDRFVDIADTSLGNDKUL-AT 240
 DB 161 YKW--FYSLOFNKESAFITGVALIASWLSQ---DESKRVVASFQGAFCGVTTFNNGFA 215

QY 241 AGIKAMLNKSDKTKI--TTDKIEINLGFVDQDSTKERLEQIAS-----KDKPS 289
 DB 216 KGLIYVQKH--KSSKIYHTSPVKLDSGF-----TAGKKNATVINNVLSSTPADVKYNPH 268

QY 290 TLAVAGPLTEIFSDIANGNDRYLIGVDTPQSLVYTKTKNKFSTILKNLGYSVFVLS 349
 DB 269 VILSVAGPAT--FETVALANKGVYIGVSDQGM--QDKDRILTSVLKAIKQAVETL 324

QY 350 DL-----YTKKSNRNLGAFERKKSATVYIGIKDRFVDIADTSLGNDKUL-AT 398
 DB 325 DLLEKEGKYPVVDKADKKMSHFGTQ-----KEKMGVLENHFSNTEQAKIN 376

QY 399 EATSEAKKEFEKTKITPAEVRKTLIEIPMPD-KQPDQOESLDKLITDINK 450
 DB 377 NKIKKAIKMKFE---LPEDFVKYINSDKALKDGNKIDNVSERLEAIISAINK 425

RESULT 13
 QYR3X3 PRELIMINARY; PRT; 428 AA.

AC Q9R3X3; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Macrophage activating lipoprotein-404 precursor.
 GN Name=malp; Synonym=malp;
 OS Mycoplasma fermentans.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 NCBI_TaxID=2115;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K7;
 RX MEDLINE=99115554; PubMed=9916088;
 RA Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
 RT "Differential posttranslational processing confers intraspecies
 variation of a major surface lipoprotein and a macrophage-activating
 lipopeptide of Mycoplasma fermentans.";
 RL Infect. Immun. 67:760-771(1999).
 DR EMBL: AF099213; AAD16397.1; -;
 DR GO: GO:0008289; F:lipid binding; IEA.
 DR InterPro: IPR003760; Bmp.
 DR InterPro: IPR008107; Mycoplasma_p48.
 DR Pfam: PF02608; Bmp; 1.
 DR PRINTS: PR01733; LIPOPROTEIN48.
 KW Lipoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 428 Potential.
 SQ SEQUENCE 428 AA; 47875 MW; C7A536B409A60132 CRC64;

Query Match 16.9%; Score 389.5; DB 2; Length 428;
 Best Local Similarity 26.8%; Pred. No. 8e-16;
 Matches 126; Conservative 99; Mismatches 176; Indels 69; Gaps 20;

QY 5 IKNNKFLGLVPLPSAI-ATISAGCWDKETEKEKSDADNQNKOITDVSKISGLVNERKS 63
 DB 1 MKKSKKILLDL-SPAILPAAVAVSCGNDES-----NISFKKXISKTTTNANGKQ 52

QY 64 EIMAAKADANKHFGNLMAIYTAGTVNDNSFNQSSWEAIQOLGALTGEITSDVSSTAE 123
 DB 53 VVKNAEL-----LKLKVLITIDESKIDKSFNQSFAELKAIKQGTGIEINNVSPS-SNF 106

QY 124 EGKYSSTANTKNVWVLSGFQHGDAFTRWLKIPENKOLFTEKNIIILIGIMTWTENV 183
 DB 107 ESAVNSALSGHKIWLNGFRHQOSIKQY--IDARELERNOIKITIGID-DIETRYK 163

QY 184 GRVYINLTYTEEAGMLAGYANASFLAKKFPSPDKRSATVYIGIKDRFVDIADTSLGNDKUL-ATEAI 243
 DB 164 --FYSLOFNKESAFITGVALIASWLSQ---DESKRVVASFQGAFCGVTTFNNGFAKGI 218

QY 244 KAMLNKSDKTKI--TTDKIEINLGFVDQDSTKERLEQIAS-----KDKPSTLL 292
 DB 219 LYYVQKH--KSSKIYHTSPVKLDSGF-----TAGKKNATVINNVLSSTPADVKYNPHVIL 271

QY 293 AVAGPLTEIFSDIANGNDRYLIGVDTPQSLVYTKTKNKFSTILKNLGYSVFVLSDL- 351
 DB 272 SVAGPAT--FETVALANKGVYIGVSDQGM--QDKDRILTSVLKAIKQAVETL 327

QY 352 -----YTKKSNRNLGAFERKKSATVYIGIKDRFVDIADTSLGNDKUL-ATEAI 401
 DB 328 LEKEGKYPVVDKADKKMSHFGTQ-----KEKMGVLENHFSNTEQAKINNKI 379

QY 402 SEAKKEFEKTKITPAEVRKTLIEIPMPD-KQPDQOESLDKLITDINK 450
 DB 380 KEAIKMKFE---LPEDFVKYINSDKALKDGNKIDNVSERLEAIISAINK 425

RESULT 14
 QYR3N6 PRELIMINARY; PRT; 428 AA.

AC Q9R3N6; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 03-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Lipoprotein MALP-404 precursor (Macrophage activating lipoprotein-404 precursor).
 GN Name=malp; Synonym=malp;
 OS Mycoplasma fermentans.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 NCBI_TaxID=2115;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PG18, M39A, and M70B;
 RX MEDLINE=99115554; PubMed=9916088;
 RA Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
 RT "Differential posttranslational processing confers intraspecies
 variation of a major surface lipoprotein and a macrophage-activating
 lipopeptide of Mycoplasma fermentans.";
 RL Infect. Immun. 67:760-771(1999).
 DR EMBL: AF100324; AAD25736.1; -;
 DR EMBL: AF099214; AAD16398.1; -;
 DR EMBL: AF099215; AAD16399.1; -;
 DR GO: GO:0008289; F:lipid binding; IEA.
 DR InterPro: IPR003760; Bmp.
 DR InterPro: IPR008107; Mycoplasma_p48.
 DR Pfam: PF02608; Bmp; 1.
 DR PRINTS: PR01733; LIPOPROTEIN48.
 KW Lipoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 38 Potential.
 SQ SEQUENCE 428 AA; 47863 MW; 59808324E218F03C CRC64;

Query Match 16.9%; Score 387.5; DB 2; Length 428;
 Best Local Similarity 26.6%; Pred. No. 1.1e-15;
 Matches 125; Conservative 101; Mismatches 175; Indels 69; Gaps 20;

QY 5 IKNNKFLGLVPLPSAI-ATISAGCWDKETEKEKSDADNQNKOITDVSKISGLVNERKS 63

```

Db      1 MKSKSKILLGL-SP1AAVLPAVAVSCGNNDSE-----NISFKKDKSKYTTNNANGKQ 52
Qy      64 EIMAKADANGHFGIINMAIVTAGTVNDNSFNQSSWEAIIQOLGALTGEIITSVDSPTAEI 123
Db      53 VKRAHEL-----LKLKPVLTIDEGKIDKSPNQAFAELKAIKQGTGIEINSVERP-SNF 106
Qy      124 EGKYSILANTNKNNWVLSGFQHGDAFTRWLKI PENKQLFTEKNIIIGIDMTDTENVIPT 183
Db      107 ESAVNSALASAGHKIIVLNGFGHQSIKQY--IDARELEBERNQIKITIGIDE-DIETEKW 163
Qy      184 GRVNLTYKTEAGMLAGYANASFLAKKFPSPDPTKRSIV--IGGGISPAVTFIAGYLAGI 243
Db      164 --FYSLQFNIKESAFTTGYALASWLSSEQ--DESKRVASFGVAFPGVTFNNGFPAKGI 218
Qy      244 KAMNLKNSDKKTKI-TTDKIEINLGFVDVDTSTKERLEQIAS-----KDKPSTLI 292
Db      219 LYVQKQK--KSKSYIHSFVLDISGF-----TAGEKMTVINNVLSSTPAVTKTNPHVYL 271
Qy      272 SVAGPAT--FETVLANKGQYVIGVSDQGMII--QDKORILTSVLKHKQAVYETLIDLII 327
Db      352 -----YTKKNSRNLAGEFEGKKSATVYLGIKDRFVIDADTSLSEGNKUL-ATBAI 401
Qy      328 LEKEEGKYPYVVKADKKKMSHFQTQ-----KEKMGVAENHPSNTEEOAKINNKI 379
Qy      402 SEAKKEFEKTKTIIPAEEFRKTLIEPEMD-KOPDKQOESLDKLTIDINK 450
Db      380 KEALIMFRE---LPEDPVKINSDKALKDGKIDNVSERLEAIIISAINK 425

```

RESULT 15

```

08RCH2 PRELIMINARY; PRT; 352 AA.
AC 08RCH2;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Surface lipoprotein.
GN Name=Med; OrderedLocusNames=TTE0457;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013017; FANM23740.1;
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR003760; Bmp.
DR Pfam; PF02608; Bmp; 1.
SQ Complete proteome; Lipoprotein.
SQ SEQUENCE 352 AA; 38052 MW; DCA7990EA271A23B CRC64;

```

Query Match 10.7%; Score 247; DB 2; Length 352;
 Best Local Similarity 25.7%; Pred. No. 3.7e-07;
 Matches 105; Conservative 62; Mismatches 161; Indels 80; Gaps 17;

```

Qy      6 KMNKFLGIVFPISATATISAGCMDEKTTKEKKSADNQNKOITDVSKISGLVNERKSEI 65
Db      3 KMRVVLASLLILIV-ALSVLISGSSK--TRQEST--QPQOTTANK-----44
Qy      66 MAARADANKHFGIINMAIVTAGTVNDNSFNQSSWEAIIQOLGALTGEIITSVDS-STAELE 124
Db      45 -----NKNF--KVGIVTVDVGINDRSFNQMAIEGLQRAKEIGVTVNVVQSOMPTDV 95

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Qy      125 GKYSILANTNKNNWVLSGFQHGDAFTRWLKI PENKQLFTEKNIIIGIDMTDTENVIPTG 184
Db      96 PNLTFNFAQCGYDLIVISGFMMHDA-----TEEVSQKFPNTKFLIIDSEITDRPNV----- 145
Qy      185 RYINLTYKTEAGMLAGYANASFLAKKFPSPDPTKRSIV--IGGGISPAVTFIAGYLAGI 242
Db      146 --ASAMFEQESVGYLAG--ALAGLVEKEKYGKYGKGINIIGAVGGMQIPPDRTFIAGYQGG 201
Qy      243 IKAMNLKNSDKKTKITTDKIEINLGFVDVDTSTKERLEQIASDKPSTLLAVAGPLTEIF 302
Db      202 AKAVN-----PDIKILINVTNNFNDPAAGKQWALNIGSGAEIIFQVAGGTGB-- 249
Qy      303 SDIT--ANQNDRYLIGVDTQOSLYTTKTKKPFSLIKNLGYSVFSVLSL-----350
Db      250 -GVIKAAQEKNLVYAIQVADADQSYL--APDNVLSAVKRYDAVAVDYIKALNNGNFKSGI 305
Qy      351 LYTKKNSRNLAGEFEGKKSATVYLGIKDRF--VDIADTSLSEGNK 394
Db      306 MYFDLKNN---GVGLKINKDVQSIIDQVNLAKDIIIDGKIQVSDK 349

```

Search completed: December 18, 2004, 01:26:31
 Job time : 131.457 secs

CC hyopneumoniae is a bacterial pathogen that causes enzootic mycoplasma pneumoniae in pigs. The mhp3 gene, proteins and apoprotein antigens of the invention are useful in the manufacture of a vaccine for treating/ preventing a disease or disorder caused by infection with M. hyopneumonae in an animal, especially a pig. The present amino acid sequence represents a mutant version of the Mycoplasma hyopneumonae mhp3 protein which was modified for expression in E. coli

SQ Sequence 423 AA;

Query Match 100.0%; Score 2155; DB 5; Length 423;

Best Local Similarity 100.0%; Pred. No. 4,2e-164; Mismatches 0; Gaps 0;

Matches 423; Conservative 0; Indels 0; Gaps 0;

QY 1 MMDKETTKEKSAQNQKQITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIYTAGGT 60
DB 1 MMDKETTKEKSAQNQKQITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIYTAGGT 60
QY 61 VNDNSFNQSGWEAIIQQLGALTGGEITSVDSSTAELEGKYSLSANTNNKVVVLSGFQHGDA 120
DB 61 VNDNSFNQSGWEAIIQQLGALTGGEITSVDSSTAELEGKYSLSANTNNKVVVLSGFQHGDA 120
QY 121 FTRMLKIPENKQLFTEKNIIILGIDMTDTEENVIPGRYINLTYTEEAGWLAGYANASFL 180
DB 121 FTRMLKIPENKQLFTEKNIIILGIDMTDTEENVIPGRYINLTYTEEAGWLAGYANASFL 180
QY 181 AKKPSDPTKSAIYIGGISPAAVDFIAGYLAGIKANLKNSDKTKITTDKIEINLGF 240
DB 181 AKKPSDPTKSAIYIGGISPAAVDFIAGYLAGIKANLKNSDKTKITTDKIEINLGF 240
QY 241 DVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANONDRYLIGVTDQSLVYTKT 300
DB 241 DVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANONDRYLIGVTDQSLVYTKT 300
QY 301 KKKFPTSLIKNLGYSVFSVSLDTYTKSNSRNLAGFEFGKKSATVYLGIKORFVDIADTS 360
DB 301 KKKFPTSLIKNLGYSVFSVSLDTYTKSNSRNLAGFEFGKKSATVYLGIKORFVDIADTS 360
QY 361 LEGNDKCLATEAISEAKKEFEKTKTIPAEVRKTLIPEMPDKQPKQOESLIDLITDI 420
DB 361 LEGNDKCLATEAISEAKKEFEKTKTIPAEVRKTLIPEMPDKQPKQOESLIDLITDI 420
QY 421 NNL 423
DB 421 NNL 423

RESULT 2
AAU01859
ID AAU01859 standard; protein; 451 AA.
XX
AC AAU01859;
XX
DT 07-SEP-2001 (first entry)
XX
DE Mycoplasma hyopneumonae MHP3 antigen.
XX
KM MHP3; antigen; vaccine; enzootic mycoplasma pneumoniae; antibody;
XX immunosassay; immunotherapy; anti-idiotypic antibody.
OS Mycoplasma hyopneumonae.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 7
FT Misc-difference 99 /note= "Encoded by TGA"
FT Misc-difference 99 /note= "Encoded by TGA"
FT Misc-difference 138 /note= "Encoded by TGA"
FT Misc-difference 152 /note= "Encoded by TGA"
FT Misc-difference 174 /note= "Encoded by TGA"
FT Misc-difference 174 /note= "Encoded by TGA"

FT Misc-difference 198
FT /note= "Encoded by TGA"
FT Misc-difference 246 /note= "Encoded by TGA"
FT
FT
FN EP1090995-A2.
XX
XX 11-APR-2001.
PD
XX
XX 26-SEP-2000; 2000EP-00308421.
PF
XX 29-SEP-1999; 99US-0156602P.
RR
XX
XX (PRIZ) PFIZER PROD INC.
PA
XX King KW, Madura RA, Rosey EJ;
PI
XX WPI: 2001-309781/33.
DR
XX N-PSDB; AAS03285.
DR
PT New apoprotein antigens encoded by mhp3 gene from Mycoplasma
PT hyopneumonae useful as a vaccine for treating or preventing diseases
PT caused by Mycoplasma hyopneumonae.
PS
PS Claim 11; Page 17-18; 38pp; English.
XX
XX The sequence is Mycoplasma hyopneumonae MHP3 antigen. MHP3 antigen and
CC its fragments are useful in manufacturing a vaccine for treating or
CC preventing a disease or disorder in an animal, especially pig, caused by
CC M. hyopneumonae infection e.g. enzootic mycoplasma pneumoniae. The mhp3-
CC encoded proteins may be used as immunogens to generate antibodies which
CC immunospecifically bind such an immunogen. The antibodies generated
CC against the antigen are useful in diagnostic immunoassays, passive
CC immunotherapy and generation of anti-idiotypic antibodies. Mhp3 proteins
CC may also be used in immunoassays, e.g. to detect or measure in a
CC biological sample from a vaccinated or potentially infected test animal
CC the presence of antibodies to the antigen, and thus to monitor the immune
CC response and/or to diagnose infection of the animal
CC
CC
SQ Sequence 451 AA;

Query Match 99.0%; Score 2134; DB 4; Length 451;

Best Local Similarity 99.8%; Pred. No. 2.2e-162; Mismatches 1; Indels 0; Gaps 0;

Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 WDKETTKESADNQNQKQITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIYTAGGT 61
DB 30 WDKETTKESADNQNQKQITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIYTAGGT 89
QY 62 NDNSFNQSGWEAIIQQLGALTGGEITSVDSSTAELEGKYSLSANTNNKVVVLSGFQHGDAF 121
DB 90 NDNSFNQSGWEAIIQQLGALTGGEITSVDSSTAELEGKYSLSANTNNKVVVLSGFQHGDAF 149
QY 122 TRMLKIPENKQLFTEKNIIILGIDMTDTEENVIPGRYINLTYTEEAGWLAGYANASFLA 181
DB 150 TRMLKIPENKQLFTEKNIIILGIDMTDTEENVIPGRYINLTYTEEAGWLAGYANASFLA 209
QY 182 KKKPSDPTKSAIYIGGISPAAVDFIAGYLAGIKANLKNSDKTKITTDKIEINLGF 241
DB 210 KKKPSDPTKSAIYIGGISPAAVDFIAGYLAGIKANLKNSDKTKITTDKIEINLGF 269
QY 242 VQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANONDRYLIGVTDQSLVYTKT 301
DB 270 VQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANONDRYLIGVTDQSLVYTKT 329
QY 302 NKFPSTSLIKNLGYSVFSVSLDTYTKSNSRNLAGFEFGKKSATVYLGIKORFVDIADTS 361
DB 330 NKFPSTSLIKNLGYSVFSVSLDTYTKSNSRNLAGFEFGKKSATVYLGIKORFVDIADTS 389
QY 362 EGNDKCLATEAISEAKKEFEKTKTIPAEVRKTLIPEMPDKQPKQOESLIDLITDI 421
DB 390 EGNDKCLATEAISEAKKEFEKTKTIPAEVRKTLIPEMPDKQPKQOESLIDLITDI 449

ID	AA015861	standard; protein; 451 AA.
XX	AA015861;	
AC		
XX		
DT	16-JAN-2003	(first entry)
XX		
DE	Mycoplasma hyopneumoniae mbp3 protein.	
XX		
KW	Apoptrotein antigen; enzootic mycoplasma pneumoniae; mbp3; vaccine;	
KM	Mycoplasma hyopneumoniae infection.	
XX		
OS	Mycoplasma hyopneumoniae.	
XX		
EH	Key	Location/Qualifiers
FT	Misc-difference 7	/note= "Encoded by TGA"
FT	Misc-difference 99	/note= "Encoded by TGA"
FT	Misc-difference 138	/note= "Encoded by TGA"
FT	Misc-difference 152	/note= "Encoded by TGA"
FT	Misc-difference 152	/note= "Encoded by TGA"
FT	Misc-difference 174	/note= "Encoded by TGA"
FT	Misc-difference 198	/note= "Encoded by TGA"
FT	Misc-difference 246	/note= "Encoded by TGA"
FT	Misc-difference 246	/note= "Encoded by TGA"
XX		
PN	EP1245677-A1.	
XX		
PD	02-OCT-2002.	
XX		
PF	30-MAR-2001; 2001EP-00303030.	
XX		
PR	30-MAR-2001; 2001EP-00303030.	
XX		
PA	(PRIZ) PRIZER PROD INC.	
PI	King KW, Madura RA, Rosey EL;	
XX		
DR	WPI; 2002-742716/81.	
DR	N-PSDB; AAL50632.	
XX		
PT	Novel apoprotein antigens encoded by Mycoplasma hyopneumoniae for use in	
PT	vaccines to prevent and treat diseases caused by infection with	
PT	Mycoplasma hyopneumoniae in animals, especially pigs.	
XX		
PS	Claim 11; Fig 1; 38pp; English.	
XX		
CC	The invention comprises the amino acid and coding sequences of Mycoplasma	
CC	hyopneumoniae mbp3 proteins, the invention also comprises novel	
CC	apoptrotein antigens encoded by the M. hyopneumoniae mbp3 gene. M.	
CC	hyopneumoniae is a bacterial pathogen that causes enzootic mycoplasma	
CC	pneumonia in pigs. The mbp3 genes, proteins and apoprotein antigens of	
CC	the invention are useful in the manufacture of a vaccine for treating/	
CC	preventing a disease or disorder caused by infection with M.	
CC	hyopneumoniae in an animal, especially a pig. The present amino acid	
CC	sequence represents a Mycoplasma hyopneumoniae mbp3 protein of the	
XX		
XX		
XX	Sequence 451 AA;	
Query Match	99.0%; Score 2134; DB 5; Length 451;	
Best Local Similarity	99.8%; Pred. No. 2.2e-162;	
Matches 419; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
07	2 WDKETKEKADNONKOITVSKISGLVNERKSEIMAKADANGHGLANMAIYTAGGTG 61	
DB	30 WDKETKEKADNONKOITVSKISGLVNERKSEIMAKADANGHGLANMAIYTAGGTG 89	

Accession	Protein	Gene	Location/Qualifiers
Qy	62	NDSFPGQSGWEAIQQGALTCGEIITSVDSSTAIEGKTSLSANTNNKVVVLSGFQHGDAF	
Db	90	NDSFPGQSGWEAIQQGALTCGEIITSVDSSTAIEGKTSLSANTNNKVVVLSGFQHGDAF	
Qy	122	TRRLKLTPEKKOLFEKKNIIILGIDMTDTEBNVIPTGRVYNLTYYTKBEAGWLAGYNASFLA	181
Db	150	TRRLKLTPEKKOLFEKKNIIILGIDMTDTEBNVIPTGRVYNLTYYTKBEAGWLAGYNASFLA	209
Qy	182	KKPSPTKRSALVIGGGISPAVDPFIAGYLAIGFANWLKNSDKKKTITTDKIEINLNGFD	241
Db	210	KKPSPTKRSALVIGGGISPAVDPFIAGYLAIGFANWLKNSDKKKTITTDKIEINLNGFD	268
Qy	242	VQDSTKERLEQIASDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVTDQSLVYTKTK	301
Db	270	VQDSTKERLEQIASDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVTDQSLVYTKTK	329
Qy	302	NKFETSIILKNLGVSVFSVLSDLYTKKNSRNLACGFEFKSAATYVLGIKDFVDIADTSL	361
Db	330	NKFETSIILKNLGVSVFSVLSDLYTKKNSRNLACGFEFKSAATYVLGIKDFVDIADTSL	389
Qy	362	EGNDKKLATEATISAEKKEFEKTKTIPAEVVRKLTLEIPEMDKQPDQKQESLQDKLITDIN	421
Db	390	EGNDKKLATEATISAEKKEFEKTKTIPAEVVRKLTLEIPEMDKQPDQKQESLQDKLITDIN	449
RESULT 4			
AAU01860			
ID	AAU01860	standard; protein; 423 AA.	
XX	AAU01860;		
AC			
DT	07-SEP-2001	(first entry)	
XX			
DE	Mycoplasma hyopneumoniae recombinant MHP3 antigen.		
XX			
KW	MHP3; antigen; vaccine; enzootic mycoplasma pneumoniae; mutant; antibody; immunotherapy; anti-idiotypic antibody; mutein.		
XX			
OS	Mycoplasma hyopneumoniae.		
XX			
EH	Key	Location/Qualifiers	
FT	Misc-difference	70	
FT		/note= "Encoded by RGA"	
FT	Misc-difference	417..422	
FT		/note= "Encoded by AATTACCGATAT"	
XX			
XX	BP1090995-A2.		
PN			
XX			
PD	11-APR-2001.		
XX			
PF	26-SEP-2000; 2000EP-00308421.		
XX			
PR	29-SEP-1999; 99US-0156602P.		
XX			
PA	(PF12) PFIZER PROD INC.		
XX			
PI	King KM, Madura RA, Rosey EL;		
XX			
DR	WPI, 2001-309781/33.		
XX			
DR	N-PSDB; AAS03286.		
XX			
PT	New apoprotein antigens encoded by mhp3 gene from Mycoplasma hyopneumoniae useful as a vaccine for treating or preventing diseases caused by Mycoplasma hyopneumoniae.		
XX			
PS	Claim 4; Page 19-21; 38pp; English.		
XX			
CC	The sequence represents Mycoplasma hyopneumoniae a recombinant MHP3 antigen lacking the first 28 amino acids (the putative signal sequence).		
CC	MHP3 antigen and its fragments are useful in manufacturing a vaccine for treating or preventing a disease or disorder in an animal, especially pig, caused by M. hyopneumoniae infection e.g. enzootic mycoplasma		

CC pneumonia. The mbp3-encoded proteins may be used as immunogens to
CC generate antibodies which immunospecifically bind such an immunogen. The
CC antibodies generated against the antigen are useful in diagnostic
CC immunosays, passive immunotherapy and generation of anti-idiotypic
CC antibodies. Mb3 proteins may also be used in immunoassays, e.g. to
CC detect or measure in a biological sample from a vaccinated or potentially
CC infected test animal the presence of antibodies to the antigen, and thus
CC to monitor the immune response and/or to diagnose infection of the animal

XX Sequence 423 AA;

Query Match 98.4%; Score 2120; DB 4; Length 423;
Best Local Similarity 100.0%; Pred. No. 2,7e-161; Indels 0; Gaps 0;
Matches 416; Conservative 0; Mismatches 0;

Qy 1 MMDKETTKEKSAONKQITDVSKISGLVNERKSEIIMAAKADANKHGLNMAIVTAGCT 60
Db 1 MMDKETTKEKSAONKQITDVSKISGLVNERKSEIIMAAKADANKHGLNMAIVTAGCT 60
Qy 61 VNDNSFNQSGWEAIQOLGALTGGETTSVDSSTAELGKYSLSANTNNKVVLSGFGHGD 120
Db 61 VNDNSFNQSGWEAIQOLGALTGGETTSVDSSTAELGKYSLSANTNNKVVLSGFGHGD 120
Qy 121 FTRWLKIPENKQLETKKIIILGIDMTENVIPGRYINLTYTEEAGMLAGYANASFL 180
Db 121 FTRWLKIPENKQLETKKIIILGIDMTENVIPGRYINLTYTEEAGMLAGYANASFL 180
Qy 181 AKKPPSPTRKSAIVIGGISPATVDFIAGYLAGIKANLKNSDKTKITTDKIEINLGF 240
Db 181 AKKPPSPTRKSAIVIGGISPATVDFIAGYLAGIKANLKNSDKTKITTDKIEINLGF 240
Qy 241 DVQDTSTYKERLEQIASKDXPSTLLAVAGPLTEIFSDIIANONDRYLIGVDTQSLVYTKT 300
Db 241 DVQDTSTYKERLEQIASKDXPSTLLAVAGPLTEIFSDIIANONDRYLIGVDTQSLVYTKT 300
Qy 301 KNKFTSTILKNLGYSVPSVLSDLTYKKSNSRLNAGFERGKSATVYIGIKRPFDIADTS 360
Db 301 KNKFTSTILKNLGYSVPSVLSDLTYKKSNSRLNAGFERGKSATVYIGIKRPFDIADTS 360
Qy 361 LEGNDKILATEAISEAKKEFEKTKTIPAEVRKTLIEIPMPDKOPDKQESLDTL 416
Db 361 LEGNDKILATEAISEAKKEFEKTKTIPAEVRKTLIEIPMPDKOPDKQESLDTL 416

RESULT 5
AAR40856
ID AAR40856 standard; protein; 453 AA.
XX
AC AAR40856;
XX
DT 25-MAR-2003 (revised)
DT 07-MAR-1994 (first entry)
XX
DE 43kd regression associated antigen.
XX
KM Regression associated antigen; tumour; immunotherapy;
XX anti-idiotypic antibodies; antibodies; tumour regression.
XX
OS Mycoplasma hyorhinis.
XX
FH Key Location/Qualifiers
FT Misc-difference 80
FT /note= "Tryptophan encoded by TGA, normal in Mycoplasma
FT hyorhinis."
FT Misc-difference 124
FT /note= "Tryptophan encoded by TGA, normal in Mycoplasma
FT hyorhinis."
FT Misc-difference 165
FT /note= "Tryptophan encoded by TGA, normal in Mycoplasma
FT hyorhinis."
FT Misc-difference 344
FT /note= "Tryptophan encoded by TGA, normal in Mycoplasma
FT hyorhinis."

XX US5242823-A.
PN 07-SEP-1993.
XX
PD 02-OCT-1992; 92US-00956546.
XX
PF 07-MAR-1986; 86US-00837494.
XX
PR 16-SEP-1987; 87US-00097910.
PR 11-DEC-1987; 87US-00131815.
PR 04-JAN-1988; 88US-00138923.
PR 16-MAR-1990; 90US-00474730.
XX
XX (ITGE-) INT GENETIC ENG INC.
XX
XX Fareed GC, Sen A, Ghosh-Dastidar P, Jar-How L;
XX WPI: 1993-295229/37.
XX DR N-PSDB; AAQ47816.
XX
XX DNA encoding a regression-associated antigen from M. hyorhinis - is used
XX to obtain prods. for diagnosis, localisation and therapy of tumours.
XX
XX Disclosure; Fig 3; 40pp; English.
XX
XX Regression associated antigens (RAA's) are identified in material from
XX neoplastic cells by their immunological reactivity with regression
XX associated antibodies from the serum of patients diagnosed as undergoing
XX regression of a tumour. RAA's can be used for tumour immunotherapy and
XX for producing and purifying antibodies which can be used for tumour
XX diagnosis, localisation and therapy. The antibodies can also be used for
XX the production of anti-idiotypic antibodies which can also be used in
XX immunotherapy. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 453 AA;

Query Match 32.6%; Score 702; DB 2; Length 453;
Best Local Similarity 38.8%; Pred. No. 1,7e-47; Indels 40; Gaps 14;
Matches 170; Conservative 82; Mismatches 146;

Qy 5 ETTKEKSAONKQITDVSKISGLVNERKSEIIMAAKADANKHGLNMAIVTAGTVNDN 64
Db 28 ETTKEKGIIT-----RIID-----NSFVDRQAIEKA-----KNDFRTVLLTAGTVQDK 73
Qy 65 SFNQSGWEAI---QOLGALTG-GETTSVDSSTAELGKYSLSANTNNKVVLSGFGHGD 119
Db 74 SFNQSIWEAVLEHVDQIEKTTNLDVSGQETNNQSELIGKYKNFLNGKNVWILTGFOGQ 133
Qy 120 AFTRWLKIPEIN-----KQLETKKIIILGIDM---TPTENVIPGRYINLTYTEEAGWL 171
Db 134 EFPKFLKQDTSNGKKYSDLAEEKVITVAVDWLSKEDKDLIKAGHFIISLYKTEAGFI 193
Qy 172 AGYANASFLAKKPPSPTRKSAIVIGGISPATVDFIAGYLAGIKANLKNSDKTKITTT 231
Db 194 AGYASSKFLAYKPPNDAKRTIAPFGGHHGAGVDFIAGYLAGIAKANNNDPTAKVITSD 253
Qy 232 DKIEINLGFVQDTSTYKERLEQIASKDXPSTLLAVAGPLTEIFSDII--ANONDRYLIGV 289
Db 254 NNINIDTGF-ISNDKTAIFNGIYNKS--SLVPEVGSLSNVDAIKKSKDKTYLIGV 310
Qy 290 DTDQSLVYTKTKKKEFFSILKNLGYSVPSVLSDLTYKKSNSRLNAGFERGK---KSATV 345
Db 311 DTDQSKIFPPA-TVFFFSIEHGLRTTYEVLTDMLKEDSKFGSFRSFLTNPNATV 369
Qy 346 YLIGKDFVPIADTSLGNDKILATEAISEAKKEFEKTKTIPAEVRKTLIEIPM--PD 403
Db 370 YKGISDFVGVSNSTVADADKVAQOFLNEBATADFKQIQANPI-NYKSYLGIFTMLIND 428
Qy 404 KQPDQOESLDTITDIN 421
Db 429 NDAKDNKALNELIKIN 446

```

RESULT 6
AA015867
ID AA015867 standard; protein; 457 AA.
XX
XX AA015867;
AC
XX
DT 16-JAN-2003 (first entry)
XX
XX Mycoplasma hyorhinis Ag234-5 protein.
DE
XX
XX Apoptoteic antigen; enzootic mycoplasma pneumoniae; mhp3; Ag234-5;
KW vaccine; Mycoplasma hyopneumoniae infection.
XX
XX Mycoplasma hyorhinis.
OS
XX
XX EP1245677-A1.
XX
XX 02-OCT-2002.
XX
XX 30-MAR-2001; 2001EP-00303030.
XX
XX 30-MAR-2001; 2001EP-00303030.
XX
XX (PF12 ) PFIZER PROD INC.
XX
XX Kling KW, Madura RA, Rosey EL;
XX
XX WPI; 2002-742716/81.
XX
XX Novel aporetic antigens encoded by Mycoplasma hyopneumoniae for use in
XX vaccines to prevent and treat diseases caused by infection with
XX Mycoplasma hyopneumoniae in animals, especially pigs.
XX
XX Example; Fig 1; 38pp; English.
XX
XX The invention comprises the amino acid and coding sequences of Mycoplasma
XX hyopneumoniae mhp3 proteins, the invention also comprises novel
XX aporetic antigens encoded by the M. hyopneumoniae mhp3 gene. M.
XX hyopneumoniae is a bacterial pathogen that causes enzootic mycoplasma
XX pneumonia in pigs. The mhp3 genes, proteins and aporetic antigens of
XX the invention are useful in the manufacture of a vaccine for treating/
XX preventing a disease or disorder caused by infection with M.
XX hyopneumoniae in an animal, especially a pig. The present amino acid
XX sequence represents the Mycoplasma hyorhinis Ag234-5 protein which is
XX shown in a figure of the invention
XX
XX
XX Sequence 457 AA;
SQ
Query Match 32.2%; Score 693.5; DB 5; Length 457;
Best Local Similarity 39.0%; Pred. No. 8.5e-47;
Matches 168; Conservative 81; Mismatches 141; Indels 41; Gaps 14;
QY 5 ETTKEESADNOKQITDVSKISGLVNERKSEIMAAKADANKHGLMAIVTAGTVNDN 64
DB 28 ETDKEGKII-----RIPD-----NSFVADKQAEIEKA-----KNDFVTVLLTAGTVQDK 73
QY 65 SFNOSGWEAI-----QOLGALTG--GEITSVDSSTAELEGKYSLSANTKNVWVLSGFGHD 119
DB 74 SFNOSIWEAEVLEHYDQIEKTNLDVSOETNOSSELGKXKNFLNGKNWVILGFGQGG 133
QY 120 AFRMLKIPEN-----QOLFTEKNIILGIDW---TOTENVIPTGRYINLTKTEAGWL 171
DB 134 EFRKFLKQTSNGKSGDLAEKVIIVAVDMDSKDKDILKQGHFISLYKTEEGGFI 193
QY 172 AGYANASFLAKKPSDPTKSAIVIGGISPAVTDFTAGIAGIKAVNLKNSDKTKITT 231
DB 194 AGYASSKFLAYKFPNDKAKRTIAPFGGSHGAGVDFIAGFIAGIAYKNNNDPTAKVITSD 253
QY 232 DKIEINLGPVQVODSTERLEQIASKDKPSTLLAVAPLPIEFSDII--ANONRYVIGV 289
DB 254 NNINIDIGP-ISKDKITFTFNGIVNKS--SLVPLVASSLTSVVDALIKSKDKTKYILGV 310
QY 290 DTDOSLVYTKKNKFTSILKNLGYSVFVSLDLVTKKNSRNLAGFEFGK---KSATV 345

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DB 311 DTDOSKIFSPA-TVFFTSIEKHIGRTIYQVLTIDWIKLEDSKFLGSRFSLTNPANATV 369
QY 346 YLIGKORFVNIADPTSLGENDKLTATEISSEAKKEPEKTKTIPAEVRKTLLEIPEM---P 402
DB 370 YKGISDPEVSVNSTVADAKVKRAQEFLEATADPFKKQIOANPT-NYKSVLGIPTMLIND 428
QY 403 DKQDPKQOESL 413
DB 429 NDAKDNEKASL 439
RESULT 7
AA067582
ID AA067582 standard; protein; 432 AA.
XX
XX AA067582;
AC
XX
XX 06-OCT-1995 (first entry)
XX
XX Cancer metastasis protein.
DE
XX
XX Cancer metastasis; clinical tests; detection.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX FT Misc-difference 55 /note= "corresponding codon TGA"
XX
XX FT Misc-difference 99 /note= "corresponding codon TGA"
XX
XX FT Misc-difference 140 /note= "corresponding codon TGA"
XX
XX FT Misc-difference 319 /note= "corresponding codon TGA"
XX
XX FT Misc-difference 420 /note= "corresponding codon TGA"
XX
XX FT Misc-difference 424 /note= "corresponding codon TGA"
XX
XX FT JF06319559-A.
XX
XX 22-NOV-1994.
XX
XX 12-MAY-1993; 93JP-00144165.
XX
XX 12-MAY-1993; 93JP-00144165.
XX
XX 12-MAY-1993; 93JP-00144165.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX WPI; 1995-040317/06.
XX
XX N-PSDB; AA079124.
XX
XX DNA encoding polypeptide involved in cancer metastasis - useful for the
XX study of the mechanism of metastasis and in clinical tests.
XX
XX Claim 1; Page 2; 13pp; Japanese.
XX
XX AA079124 encodes AA067582 a protein involved in cancer metastasis, which
XX may be used for the study of metastatic mechanisms, and for clinical tests
XX to determine the presence or absence of cancer metastasis
XX
XX Sequence 432 AA;
SQ
Query Match 32.1%; Score 692.5; DB 2; Length 432;
Best Local Similarity 39.0%; Pred. No. 9.4e-47;
Matches 168; Conservative 81; Mismatches 141; Indels 41; Gaps 14;
QY 5 ETTKEESADNOKQITDVSKISGLVNERKSEIMAAKADANKHGLMAIVTAGTVNDN 64
DB 3 ETDKEGKII-----RIPD-----NSFVADKQAEIEKA-----KNDFVTVLLTAGTVQDK 48
QY 65 SFNOSGWEAI-----QOLGALTG--GEITSVDSSTAELEGKYSLSANTKNVWVLSGFGHD 119

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Db 49 SFNQSWEAVLEHYDQIEKTNLDRVSOETNNOSELIGKYKNFLNGKNWILTFQOQG 108
Qy 120 AFTWMLKIPEN-----KQLFTEKNIIILGIDW--TDTENVIPTRGYINTLYKTEBAGWL 171
Db 109 EFPKFLKQTDNSNGKYSDLAEKKVILVAVDWDLSKEDKDLKAGHIFSLYKTEBAGFI 168
Qy 172 AGVANASFLAKKPPSPDPTKRSALVIGGISPAYTDPIAGIAGIKAMNLKNSDKTKITTT 231
Db 169 AGYASSKFLAYKFPNDEAKRTIAPFGGAGVTDPIAGIAGIAGIKAMNLKNSDKTKITTT 228
Qy 232 DKIEINQPDVODSTYKTERLEQJASKKPSLTLAVAGLEIFSDII--ANONRYILGV 289
Db 229 NNINIDTGF-LSNKTATFINGIVNKS--SLVLPVAGSLTSSVVDALIKSKKDTKYLLGV 285
Qy 290 DTDOSLVTYTKNKFSTSIILKNLGYSVPSVLSDLTYTKSNSRNLAGFEFGK---KSATV 345
Db 286 DTDOSKIFSPA-TYFFTSIEHGLRTIYQVLTIDWLKEDSKFLGSPRSFKLTTPANATV 344
Qy 346 YLGIKDRFVDIADTSLSEGNDRKCLATEAISAKKEFEEXTKTIIPAEVARKTLEIDEM--P 402
Db 345 YKGISDFFGVSNSTVADADKVKAOEFLNEATADFCKQIQANPT-NYKSVLGIFPTMLIND 403
Qy 403 DKQPDKQOESL 413
Db 404 NDARKNEKASL 414

RESULT 8

AAP93343 ID AAP93343 standard; protein; 448 AA.

AAP93343;

DT 25-MAR-2003 (revised)
DT 01-AUG-1990 (first entry)DE Gene encoding the 43 kd regression-associated antigen (RA Ag) of
Mycoplasma hyorhinis.KW Tumour regression-associated antigens (RA Ag): in vivo imaging;
therapy monitoring; cancer therapy; Mycoplasma hyorhinis.

OS Mycoplasma hyorhinis.

FH Key Location/Qualifiers
FT Peptide 1..25
FT Protein 26..448

PN EPJ08265-A.

PD 22-MAR-1989.

PE 16-SEP-1988; 88EP-00308625.

PR 16-SEP-1987; 87US-00097910.

PR 11-DEC-1987; 87US-00131815.

PA (ITGE-) INT GENETIC ENG INC.

PA (INGE-) INGENE INT GENETIC.

PI Fareed GC, Sen A, Ghoshdasti P, Li A, Lee JH;

WPI; 1989-087638/12.

DR N-PSDB; AAN90684.

PT Tumour regression-associated antigens and antibodies - used in diagnostic
tests, monitoring course of therapy and for therapy in cancer patients.

PS Disclosure; Page 7; 56pp; English.

CC Regression-associated antigens may be used in diagnostic tests, eg in

CC vivo imaging, for monitoring the course of therapy or for therapeutic
CC purposes, eg active immunisation protocols in cancer patients or drug
CC delivery systems by binding the drug to monoclonal or monospecific
CC polyclonal Ab showing specific immunoreactivity with the Ag. (Updated on
CC 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
CC field.)

SQ Sequence 448 AA;

Query Match 29.8%; Score 642.5; DB 1; Length 448;
Best Local Similarity 38.0%; Pred. No. 1e-42;
Matches 166; Conservative 83; Mismatches 145; Indels 43; Gaps 18;

Qy 5 ETTKEKSNQNKQITDVSIGSLVNERSEIMAAADANKHGLMAIVTAGTINDN 64

Db 28 ETDDEGKII-----RIPD-----NSFVDRQAEIEKA-----KNDFNTVLLTAGTVQDK 73

Qy 65 SFNQSWEAVLEHYDQIEKTNLDRVSOETNNOSELIGKYKNFLNGKNWILTFQOQG 119

Db 74 SFNQSWEAVLEHYDQIEKTNLDRVSOETNNOSELIGKYKNFLNGKNWILTFQOQG 133

Qy 120 AFTWMLKIPEN-----KQLFTEKNIIILGIDW--TDTENVIPTRGYINTLYKTEBAGWL 171

Db 134 EFPKFLKQTDNSNGKYSDLAEKKVILVAVDWDLSKEDKDLKAGHIFSLYKTEBAGFI 193

Qy 172 AGVANASFLAKKPPSPDPTKRSALVIGGISPAYTDPIAGIAGIAGIKAMNLKNSDKTKITTT 231

Db 194 AGYASSKFLAYKFPNDEAKRTIAPFGGAGVTDPIAGIAGIAGIKAMNLKNSDKTKITTT 253

Qy 232 DKIEINQPDVODSTYKTERLEQJASKKPSLTLAVAGLEIFSDII--ANONRYILGV 289

Db 254 NNINIDTGF-LSNKTATFINGIVNKS--SLVLPVAGSLTSSVVDALIKSKKDTKYLLGV 310

Qy 290 DTDOSLVTYTKNKFSTSIILKNLGYSVPSVLSDLTYTKSNSRNLAGFEFGK---KSATV 345

Db 311 DTDOSKIFSPA-TYFFTSIEHGLRTIYQVLTIDWLKEDSKFLGSPRSFKLTTPANATV 367

Qy 346 YLGIKDRFVDIADTSLSEGNDRKCLATEAISAKKEFEEXTKTIIPAEVARKTLEIDEM-PDK 404

Db 368 YKGISD-FLGVSNSTVADADKVKAOEFLN-ATADFCKQIQANPT-NYKSVLGIFPTMLIND 424

Qy 405 QPDKQOESLDTIDIN 421

Db 425 DAKNERALNELIKIN 441

RESULT 9

AAY05332 ID AAY05332 standard; peptide; 428 AA.

AAY05332;

DT 25-JUN-1999 (first entry)

DE Inflammatory cytokine inducer.

KW Inflammatory cytokine inducer; thrombocytopaenia; therapy.

OS Synthetic.

PN JPI1089582-A.

PD 06-APR-1999.

PE 19-SEP-1997; 97JP-00273649.

PR 19-SEP-1997; 97JP-00273649.

PR (CHUS) CHUGAI PHARM CO LTD.

WPI; 1999-281057/24.

DR N-PSDB; AAX33847.

PT New inflammatory cytokine inducer gene and polypeptide - useful for
PT treatment of thrombocytopenia.

PS Claim 3, Page 16-17, 22pp; Japanese.

XX This sequence represents the inflammatory cytokine of the invention. The
CC inflammatory cytokine can be used in a drug, which is useful for the
CC treatment of thrombocytopenia

XX Sequence 428 AA:

Query Match 17.6%; Score 379.5; DB 2; Length 428;
Best Local Similarity 26.7%; Pred. No. 1.2e-21;
Matches 115; Conservative 88; Mismatches 156; Indels 71; Gaps 17;

QY 31 NERKSEIMAKADANKH-----FGLNMAIVTAGTYNDNSFNQSGWEAI 74
DB 27 NNDSESNISFKEKIDSKYTTTNANGQVYKNAELLKLPVLTDEGKIDDSFNQSAFEAL 86
QY 75 QOLGALTGETSTVDSSTAELEGYSSLANTKNKNVWVLSGFQHGDAFTRWLKIPEKOLF 134
DB 87 KAIKQGTGIEINNVES--SNFESAYNSALSAGHKIWLNGFKQOSIKQY--IDAHEBEL 143
QY 135 TEKNIIILGIDWTDENVIPTRGRYINLTYTEAGWLAGYANASFLAKKPESDPTKSAI 194
DB 144 ERNQIKIIGIDF-DIETEVK--FYSLOFNKESAFITGYALMSLEQ--DESKVVA 197
QY 195 VIGGGSIPATVDFIAGIAGIKAMNLKNSDKTKI--TTDKIEINLGFVDVDTSTKERLEQ 253
DB 198 SFGGGAFFGYTTTFEGAKGLIYVNOGR--KSKIIYHTSPVKLDSGF--TAGKKMNT 250
QY 254 IAS-----KDKPSTLLAVAGPLTEIFPSDIIANONDRYLIGVTDQSLVYTKRNK 303
DB 251 VINNVLSSTPADVYKYNPHVILSVAGPAT--FETVRLANKQGYVIGVSDQGM--QDKDR 306
QY 304 FFSILKNLGSVPSVLSL-----YTKKSNRNLAGFEFGKKSATVYLGIDRF 353
DB 307 ILTSVLKHIOAVYETLLDILEKEGKPYVVKDKKADKWSHFQO-----KEKW 358
QY 354 VDIADTSLGNDDKL-ATEAISEAKKEFEKTKTTPAEVRYKTLIEIMPD-KQPDQOE 411
DB 359 IGVAENHFSNTEBQAKINNKIKAIKMFKE---LPEDFVKYINSKALDKGNKIDVSE 414
QY 412 SLDKLITDIN 421
DB 415 RLEKATISAIN 424

RESULT 10
ID ABP71709 standard; protein; 428 AA.

AC ABP71709;

DT 04-APR-2003 (first entry)

XX M161 antigen amino acid sequence.

XX M161; antigen; cytotoxic T-lymphocyte inducer; CTL; cytostatic; cancer;
KM anticancer agent.

XX Mycoplasma fermentans.

OS Key Location/Qualifiers

PH M161 difference 121 /note= "Encoded by TGA; unexplained stop codon in coding
sequence"

FT M161 difference 163 /note= "Encoded by TGA; unexplained stop codon in coding
sequence"

FT M161 difference 185 /note= "Encoded by TGA; unexplained stop codon in coding
sequence"

FT M161 difference 185 /note= "Encoded by TGA; unexplained stop codon in coding
sequence"

FT Misc-difference 348 /note= "Encoded by TGA; unexplained stop codon in coding
sequence"

FT Misc-difference 358 /note= "Encoded by TGA; unexplained stop codon in coding
sequence"

XX WO2002102402-A1.

XX 27-DEC-2002.

XX 13-JUN-2002; 2002WO-JP005916.

XX 15-JUN-2001; 2001JP-00182250.

XX (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 2003-167451/16.

XX N-PSDB; AB259715.

XX M161 antigen, its peptide fragment or their salt with e.g. superior CTL-
inductive effect, applicable in anticancer agents combined with cancer
antigen for preventing or treating cancer.

XX Disclosure; Fig 1, 94pp; Japanese.

XX The invention relates to cytotoxic T-lymphocyte (CTL)-inducers containing
the M161 antigen, its partial peptide or their salt. The activity of CTL-
inducers of the invention may be described as cytostatic. The antigen or
its peptide fragment are applicable in anticancer agents for the
prevention or treatment of cancer. The antigen and its derivative have
superior CTL-inductive effect, giving anticancer agents that have low
toxicity. The current sequence represents the M161 antigen amino acid
sequence

XX Sequence 428 AA:

Query Match 17.6%; Score 379.5; DB 6; Length 428;
Best Local Similarity 26.7%; Pred. No. 1.2e-21;
Matches 115; Conservative 88; Mismatches 156; Indels 71; Gaps 17;

QY 31 NERKSEIMAKADANKH-----FGLNMAIVTAGTYNDNSFNQSGWEAI 74
DB 27 NNDSESNISFKEKIDSKYTTTNANGQVYKNAELLKLPVLTDEGKIDDSFNQSAFEAL 86
QY 75 QOLGALTGETSTVDSSTAELEGYSSLANTKNKNVWVLSGFQHGDAFTRWLKIPEKOLF 134
DB 87 KAIKQGTGIEINNVES--SNFESAYNSALSAGHKIWLNGFKQOSIKQY--IDAHEBEL 143
QY 135 TEKNIIILGIDWTDENVIPTRGRYINLTYTEAGWLAGYANASFLAKKPESDPTKSAI 194
DB 144 ERNQIKIIGIDF-DIETEVK--FYSLOFNKESAFITGYALMSLEQ--DESKVVA 197
QY 195 VIGGGSIPATVDFIAGIAGIKAMNLKNSDKTKI--TTDKIEINLGFVDVDTSTKERLEQ 253
DB 198 SFGGGAFFGYTTTFEGAKGLIYVNOGR--KSKIIYHTSPVKLDSGF--TAGKKMNT 250
QY 254 IAS-----KDKPSTLLAVAGPLTEIFPSDIIANONDRYLIGVTDQSLVYTKRNK 303
DB 251 VINNVLSSTPADVYKYNPHVILSVAGPAT--FETVRLANKQGYVIGVSDQGM--QDKDR 306
QY 304 FFSILKNLGSVPSVLSL-----YTKKSNRNLAGFEFGKKSATVYLGIDRF 353
DB 307 ILTSVLKHIOAVYETLLDILEKEGKPYVVKDKKADKWSHFQO-----KEKW 358
QY 354 VDIADTSLGNDDKL-ATEAISEAKKEFEKTKTTPAEVRYKTLIEIMPD-KQPDQOE 411
DB 359 IGVAENHFSNTEBQAKINNKIKAIKMFKE---LPEDFVKYINSKALDKGNKIDVSE 414
QY 412 SLDKLITDIN 421

Db	415	RLBAITSAIN 424
		RESULT 11
		ADK68536
XX	ID	ADK68536 standard, protein; 404 AA.
XX	AC	ADK68536;
XX	DT	06-MAY-2004 (first entry)
XX	XX	Mycoplasma fermentans IL-X mature protein #1.
XX	XX	Immunoregulatory factor; IL-X; lymphocyte proliferation.
XX	OS	Mycoplasma fermentans.
XX	PN	US6506892-B1.
XX	PD	14-JAN-2003.
XX	PF	29-OCT-1998; 98US-00182625.
XX	PR	29-OCT-1997; 97US-0063701P.
XX	PA	(WEBB/) WEBB A C.
XX	PA	(BLAZ/) BLAZAR B A.
XX	PI	Webb AC, Blazar BA;
XX	XX	WPI; 2003-401108/38.
XX	DR	N-PSDB; ADK68530.
XX	PT	New isolated polynucleotide, useful for augmenting proliferation of B and T lymphocytes.
XX	PS	Claim 12; SEQ ID NO 14; 42PP; English.
XX	CC	The invention provides novel immunoregulatory factor designated IL-X
XX	CC	which has been isolated Mycoplasma and polynucleotides encoding such
XX	CC	polypeptides. The polynucleotide is useful for augmenting proliferation
XX	CC	of B and T lymphocytes. The present sequence is Mycoplasma fermentans IL-
XX	CC	X mature protein.
XX	XX	
SQ	Sequence	404 AA;
	Query Match:	17.6%; Score 378.5; DB 7; Length 404;
	Best local Similarity	26.7%; Pred. No. 1.3e-21;
	Matches 115; Conservative	88; Mismatches 156; Indels 71; Gaps 17;
QY	31	NERKSEIMAAKADAKH-----FGANMAIVTAGGVNDNSFNOSGWEAI 74
Db	3	NNDESNISFKEKDIDSKYTTTANGQVYKNAEMLKLKPLITIDBKIDKSPNOSAFEL 62
QY	75	QQLGALTGEITSVDSSTAELGKYSLSANTNNKVVWVLSGFQHGDAFTRLKIPENKOLF 134
Db	63	KAINKOTGEIINNVPSS-SNFESAYNALSAGHKIWLNGFRHQGSIKQY-IDAHREEL 119
QY	135	TEKNIIIGIDMTDPIENAVIPGCRYINLTYKTEBAGWLAGYANASFLAKKFPSPDPTKESAI 194
Db	120	ERNQIKIIGIDF-DIETERYKW--FYSLQFNIKESAFTTGIVYALASLSBO--DESKRVVA 173
QY	195	VIGGISPAVTFPIAGYLAGIKANMLKNSDKTKTI-TTDKIEINLGFVQDTSTKERLEQ 253
Db	174	SFGGGAFFGVTFTFNNGFAKGIILYNQKH--KSSKIYHTSPVGLDSCF-----TAGEKNWT 226
QY	254	IAS-----KDPSTLLAVAGPLTEIFSDIIANONDRYLIVDPDQSLVYTKTKNK 303
Db	227	VINNVLSTPADVKKXNPHVILSVAPAR--PFTVALANKGVIVIGVSDQGM-I--QDDDR 282
QY	304	PFTSILIKNLGVSVESVLSDL-----YTKKSNRNLAGFEFGKSAIVYIGIKORF 353
Db	283	ILTVSLTKHIKQAVVETLLDLILEKEGYKPYVVKDKKADKWSHGTO-----KEKW 334

QY	354	VDIADTSLSEGNDKLI-ATPAISSEAKCFEPEKTKTTPAEEVYKTLLEIPKMD-KQDPKQGE	411
DB	335	IGVAENHPSNTPEQAKINNKIKKAIKMFKE---LPEDFVKYINSDKALKDGNKIDNVSE	390
QY	412	SUDKLITDIN	421
DB	391	RLEAITSAIN	400
RESULT 12			
ID	ADK68531	standard; protein; 428 AA.	
XX	ADK68531;		
XX	AC		
XX	DT		
XX	06-MAY-2004	(first entry)	
XX	DE	Mycoplasma fermentans IL-X precursor protein #1.	
XX	KW	Immunoregulatory factor; IL-X; lymphocyte proliferation.	
XX	OS	Mycoplasma fermentans.	
XX	XX		
FH	Key	Location/Qualifiers	
FT	Peptide	1..24	
FT	Protein	/label= Signal_peptide	
FT		25..428	
FT		/note= "Mature IL-X protein"	
XX	PN	US6506892-B1.	
XX	XX		
PD	14-JAN-2003.		
XX	PF	29-OCT-1998; 98US-00182625.	
XX	PR	29-OCT-1997; 97US-0063701P.	
XX	PA	(WEBB/) WEBB A C.	
XX	PI	(BLAZ/) BLAZAR B A.	
XX	PI	Webb AC; Blazar BA;	
XX	DR	WPI: 2003-401108/38.	
XX	XX	N-PsDB; ADK68530.	
XX	XX		
XX	PS	Claim 25; SEQ ID NO 9; 42pp; English.	
XX	CC	The invention provides novel immunoregulatory factor designated IL-X	
XX	CC	which has been isolated Mycoplasma and polynucleotides encoding such	
XX	CC	polypeptides. The polynucleotide is useful for augmenting proliferation	
XX	CC	of B and T lymphocytes. The present sequence is Mycoplasma fermentans IL-	
XX	XX	X precursor protein.	
QY	Sequence 428 AA;		
QY	Query Match	17.6%; Score 378.5; DB 7; Length 428;	
DB	Best Local Similarity	26.7%; Pred. No. 1.4e-21;	
DB	Matches 115; Conservative	88; Mismatches 156; Indels 71; Gaps 17	
QY	31	NERKSEIIMAAKADANKH-----FGLMAIYTAGGTVDNDSNOSGWEAI	74
DB	27	NNDENISIFKEKDISKYTTTANGKQVKNMELKIKPLITDEGKIDKSFNOSAFEL	86
QY	75	QOLGALTGEIRTSVDSSTAELGKYSLSANTKQWVLSGFOHGDATFRWLKIPENKOLF	134
DB	87	KAINKOTGELINNVEPS-SNFESAYNSALSAGHKIWLNGFTHQOSIKOY--IDAREEL	143
QY	135	TEKNIIIGIDWTDTEENVIPTGRYINLTLYKTEBAGMLAGYANASFLAKKFPSPDPTKRSAT	194

Db 144 ERNOIKIGIDF-DIETRYKM--FYSLOFNKESAFITGVALASWLSQ---DESKRVA 197
 QY 195 VIGGGISPAVTDPLAGLAGIKAMNLSKSDKTKI--TTDKIEINLGFVDQSTKERLEQ 253
 Db 198 SFGGGAFFGVITTFEGRAKGLIYNQKH--KSKITHTSPVKLDSGF-----TAGEMANT 250
 QY 254 IAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDSLVTYTKTKNK 303
 Db 251 VINNVLSSTPADVAKYNPHVILSVAGPAT--FETVRLANKQGYIVGVDSDQGM1--QDKDR 306
 QY 304 FFFSILKNLGYSPFSVLSDL-----YTKNSNRNLAGEFFGKKSATVYIGIDRF 353
 Db 307 ILTSVLGHIRKQAVETLIDLILKEKEGKPYVVDKXADKKWSHFQTQ-----KEKW 358
 QY 354 VDIADTSLSEGNDDKL-ATEAISEAKKEFEKTKTIPAEVRYKTLIEIPMPD-KQPDKQOE 411
 Db 359 IGVAENHFSTBERQAKINNKIKKAIKMFKE---LPEDFVKYINSDKALDKGNKIDNVSE 414
 QY 412 SLDKLITDIN 421
 Db 415 RLEALISAIN 424

RESULT 13

ADK68537 ID ADK68537 standard; protein; 404 AA.

AC ADK68537;

XX 06-MAY-2004 (first entry)

XX Mycoplasma fermentans IL-X mature protein #2.

XX Immunoregulatory factor; IL-X; lymphocyte proliferation.

XX Mycoplasma fermentans.

XX US6506892-B1.

XX 14-JAN-2003.

XX PF 29-OCT-1998; 98US-00182625.

XX PR 29-OCT-1997; 97US-0063701P.

XX PA (WEBB/) WEBB A C.

XX PA (BLAZ/) BLAZAR B A.

XX PI Webb AC, Blazar BA;

XX WPI; 2003-401108/38.

XX N-PSDB; ADK68535.

XX New isolated polynucleotide, useful for augmenting proliferation of B and T lymphocytes.

XX PS Claim 13; SEQ ID NO 15; 42pp; English.

XX CC The invention provides novel immunoregulatory factor designated IL-X

XX CC which has been isolated Mycoplasma and polynucleotides encoding such

XX CC polypeptides. The polynucleotide is useful for augmenting proliferation

XX CC of B and T lymphocytes. The present sequence is Mycoplasma fermentans IL-

XX CC X mature protein.

XX SQ Sequence 404 AA;

QY Query Match 17.4%; Score 375.5; DB 7; Length 404;

Db Best Local Similarity 26.7%; Pred. No. 2.3e-21;

Matches 115; Conservative 87; Mismatches 157; Indels 71; Gaps 17;

31 NERKSEITMAKADANKI-----FGLMAITTAGTGVNDNSFNQSGWEAI 74

3 NNDSENSISFEKDISKYTTTNGANGQVKNALKLKPLITIDEGKIDDKSFNOSAFEL 62

QY 75 QQTALGTGEITVSSTAELEKYSLSANTNKNVWLSGFOHGDAPTRMLKIPENKOLF 134
 Db 63 KALNKQIGIEINNVEPS-SNFESAYNSALSAHKIWLNGFKHQOSIKQY--IDAYNEEL 119
 QY 135 TENKIITLIGDWDTEIVITGRYINLTYTEBAGLAGAANASFLAKKPPSPDTKSAI 194
 Db 120 ERNOIKIGIDF-DIETRYKM--FYSLOFNKESAFITGVALASWLSQ---DESKRVA 173
 QY 195 VIGGGISPAVTDPLAGLAGIKAMNLSKSDKTKI--TTDKIEINLGFVDQSTKERLEQ 253
 Db 174 SFGGGAFFGVITTFEGRAKGLIYNQKH--KSKITHTSPVKLDSGF-----TAGEMANT 226
 QY 254 IAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDSLVTYTKTKNK 303
 Db 227 VINNVLSSTPADVAKYNPHVILSVAGPAT--FETVRLANKQGYIVGVDSDQGM1--QDKDR 282
 QY 304 FFFSILKNLGYSPFSVLSDL-----YTKNSNRNLAGEFFGKKSATVYIGIDRF 353
 Db 283 ILTSVLGHIRKQAVETLIDLILKEKEGKPYVVDKXADKKWSHFQTQ-----KEKW 334
 QY 354 VDIADTSLSEGNDDKL-ATEAISEAKKEFEKTKTIPAEVRYKTLIEIPMPD-KQPDKQOE 411
 Db 335 IGVAENHFSTBERQAKINNKIKKAIKMFKE---LPEDFVKYINSDKALDKGNKIDNVSE 390
 QY 412 SLDKLITDIN 421
 Db 391 RLEALISAIN 400

RESULT 14

ADK68538 ID ADK68538 standard; protein; 428 AA.

AC ADK68538;

XX 06-MAY-2004 (first entry)

XX Mycoplasma fermentans IL-X precursor protein #2.

XX Immunoregulatory factor; IL-X; lymphocyte proliferation.

XX Mycoplasma fermentans.

XX Key Location/Qualifiers

XX Peptide 1..24

XX Protein /label= Signal_peptide

XX /note= "Mature IL-X protein"

XX US6506892-B1.

XX 14-JAN-2003.

XX PF 29-OCT-1998; 98US-00182625.

XX PR 29-OCT-1997; 97US-0063701P.

XX PA (WEBB/) WEBB A C.

XX PA (BLAZ/) BLAZAR B A.

XX PI Webb AC, Blazar BA;

XX WPI; 2003-401108/38.

XX N-PSDB; ADK68535.

XX New isolated polynucleotide, useful for augmenting proliferation of B and T lymphocytes.

XX Claim 26; SEQ ID NO 16; 42pp; English.

XX The invention provides novel immunoregulatory factor designated IL-X

XX which has been isolated Mycoplasma and polynucleotides encoding such

CC polypeptides. The polynucleotide is useful for augmenting proliferation
 CC of B and T lymphocytes. The present sequence is Mycoplasma fermentans IL-
 CC X precursor protein.

XX Sequence 428 AA;

Query Match 17.4%; Score 375.5; DB 7; Length 428;
 Best Local Similarity 26.7%; Pred. No. 2.5e-21;
 Matches 115; Conservative 87; Mismatches 157; Indels 71; Gaps 17;

QY 31 NERSEIMAAKADANKH-----FGLMAIYTAGTVNDNSFNQGEAI 74
 DB 27 NNDNSNISFEKDKISKYTTTANAGKQVNAELKLKPLITDDESKIDDKSPNOSAFEL 86
 QY 75 QQLGALTGGEITVSSTAELEGKXSSLANTKNVVWVLSGFQHDAPFRMLKIPENKOLF 134
 DB 87 KAIKQKQIEINNVEPS-SNFESAYNSALSGHKIMVNGFKHQOSIKQY--IDAYREEL 143
 QY 135 TEKNIILIGIDMTENVIPTRYINLTYTEEGWLAGYANASFLAKKPPSDPTKSAI 194
 DB 144 ERNOKIKIGIDF-DIEFEYK--FVSLQFNKESAFITGVAIASWLSQ--DESKRVVA 197
 QY 195 VIGGISPATVDTFIAGYLAGIKAMNLSKDKTKI-TTDKIEINLGPVDSTKRELEQ 253
 DB 198 SFGGGAFFGVTTNEGFAKGLITYNQKH--KSKITYHTSPVKLDSGF-----TAGEKMT 250
 QY 254 IAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVTDQSLVYTKTKNK 303
 DB 251 VINNVLSSTPADVKNPHVILSVAGPAT--PEYVRLANKGGYVIGVSDQGM--QDKDR 306
 QY 304 FFFSILKMLGYSVPSVSLD-----YTKKSNRNLAGEFGKKSATVYIGIDRF 353
 DB 307 ILTSTVLKRIKQAVYETLIDLLEKEBGKPPVVDKKADKKMSHFGTQ-----KEKW 358
 QY 354 VIDIDTSLGNDKTL-ATEAISEAKKEFEKTKTTPAEVVKTLIEIPMPD-KOPDQOE 411
 DB 359 IGVENHPSNTEBOAKINNKIKAIKMFKE---LPEDFVYINSKALKGKNKIDNVSE 414
 QY 412 SLDKLTIDIN 421
 DB 415 RLEAIIISAIN 424

RESULT 15
 AAM22727 standard; protein; 429 AA.

XX AAM22727;

XX 26-FEB-1998 (first entry)

XX Membrane protein M161Ag.

XX M161Ag; membrane protein; leukaemia; treatment.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 121 /note= "selenocysteine"

XX Modified-site 163 /note= "selenocysteine"

XX Modified-site 185 /note= "selenocysteine"

XX Modified-site 348 /note= "selenocysteine"

XX Modified-site 358 /note= "selenocysteine"

XX JF09157295-A.

XX 17-JUN-1997.

PF 05-DEC-1995; 95UP-00344504.

XX 05-DEC-1995; 95UP-00344504.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 1997-369470/34.

XX N-PSDB; AAT75133.

XX Membrane protein M161Ag - useful in development of leukaemia treating agent.

PS Claim 1; Fig 1; 6pp; Japanese.

CC This sequence is a membrane protein designated M161Ag. Oligonucleotide
 CC probes for the cDNA were designed from putative N-terminal M161Ag peptide
 CC sequences isolated from P39 cells. M161Ag can be used in the development
 CC of a leukaemia treating agent

XX Sequence 429 AA;

Query Match 17.3%; Score 372; DB 2; Length 429;
 Best Local Similarity 26.8%; Pred. No. 4.8e-21;
 Matches 117; Conservative 88; Mismatches 167; Indels 64; Gaps 18;

QY 13 ADNONKOIT---DVSKISGLVNERKSEIMAAKADANKHFGMAIYTAGTVNDNSFNQ 68
 DB 26 ANNDNSNISFEKDKISKYTTTANAGKQVNAEL-----LKLKPLITDDESKIDDKSPN 80
 QY 69 SCWEAIOQLGALTGGEITVSSTAELEGKXSSLANTKNVVWVLSGFQHDAPFRMLKIP 128
 DB 81 SAFALKAIKQKQIEINNVEPS-SNFESAYNSALSGHKIMVNGFKHQOSIKQY--ID 137
 QY 129 ENKOLFTEKNIILIGIDMTENVIPTRYINLTYTEEGWLAGYANASFLAKKPPSDP 188
 DB 138 AHRELEERNQIKIIGIDF-DIEFEYK--FVSLQFNKESAFITGVAIASWLSQ--DE 191
 QY 189 TKGSAIIVGGISPAVDTFIAGYLAGIKAMNLSKDKTKI-TTDKIEINLGPVDST 247
 DB 192 SKRVVAFSGGAFPGVTTNEGFAKGLITYNQKH--KSKITYHTSPVKLDSGF-----TA 244
 QY 248 KERLEQIAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVTDQSLV 297
 DB 245 GERKNIVINNVLSTPADVKNPHVILSVAGPAT--PEYVRLANKGGYVIGVSDQGM-- 301
 QY 298 TKTNKEFFSILKMLGYSVPSVSLD-----YTKKSNRNLAGEFGKKSATVYL 347
 DB 302 -QDKDRILTSTVLKRIKQAVYETLIDLLEKEBGKPPVVDKKADKKXSHFGTQ----- 354
 QY 348 GIKDRFVIDTSLGNDKTL-ATEAISEAKKEFEKTKTTPAEVVKTLIEIPMPD-KQ 405
 DB 355 --KEKXIGVABNOFSNTEBOAKINNKIKAIKMFKE---LPEDFVYINSKALKGKNK 408
 QY 406 PDKQESLDLTIDIN 421
 DB 409 IDNVSERLEAIIISAIN 424

Search completed: December 18, 2004, 01:22:25
 Job time : 112.476 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2004, 01:16:03 ; Search time 29.0389 Seconds
(without alignments)
966.032 Million cell updates/sec

Title: US-09-676-249D-4
Perfect score: 2155
Sequence: 1 MMDEKTTKEKSDNQNKQI.....KPDKQESLDKLTIDNNL 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A COMB.pdp: *
2: /cgn2_6/ptodata/1/1aa/5B COMB.pdp: *
3: /cgn2_6/ptodata/1/1aa/6A COMB.pdp: *
4: /cgn2_6/ptodata/1/1aa/6B COMB.pdp: *
5: /cgn2_6/ptodata/1/1aa/6C COMB.pdp: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pdp: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	378.5	17.6	404	US-09-182-625F-14	Sequence 14, Appl
2	378.5	17.6	428	US-09-182-625F-9	Sequence 9, Appl
3	375.5	17.4	404	US-09-182-625F-15	Sequence 15, Appl
4	375.5	17.4	428	US-09-182-625F-16	Sequence 16, Appl
5	204	9.5	363	US-09-583-110-2686	Sequence 2686, Ap
6	202	9.4	328	US-08-961-083-8	Sequence 8, Appl
7	202	9.4	328	US-09-536-784-8	Sequence 8, Appl
8	202	9.4	374	US-09-107-532A-5084	Sequence 5084, Ap
9	178	8.3	339	US-09-071-035-80	Sequence 80, Appl
10	178	8.3	341	US-08-396-957A-5	Sequence 5, Appl
11	178	8.3	361	US-09-071-035-78	Sequence 78, Appl
12	178	8.3	375	US-09-134-000C-6005	Sequence 6005, Ap
13	174	8.1	362	US-09-134-000C-6004	Sequence 6004, Ap
14	173	8.0	166	US-09-182-625F-6	Sequence 6, Appl
15	161	7.5	339	US-08-396-957A-4	Sequence 4, Appl
16	143	6.6	353	US-08-313-412-1	Sequence 1, Appl
17	137.5	6.4	889	US-09-952-267B-15	Sequence 15, Appl
18	137.5	6.4	889	US-09-952-267B-15	Sequence 15, Appl
19	136	6.3	553	US-09-134-001C-2974	Sequence 2974, Ap
20	133	6.2	867	US-08-973-462-8	Sequence 8, Appl
21	133	6.2	867	US-09-540-236-2676	Sequence 2676, Ap
22	127.5	5.9	518	US-09-248-796A-18238	Sequence 18238, A
23	121.5	5.6	1073	US-09-206-942-49	Sequence 49, Appl
24	121.5	5.6	1079	US-09-206-942-47	Sequence 47, Appl
25	119.5	5.5	834	US-09-187-999-11	Sequence 11, Appl
26	119	5.5	878	US-09-540-236-3401	Sequence 3401, Ap
27	119	5.5	2285	US-09-308-375-2	Sequence 2, Appl

28	117.5	5.5	1098	1	US-08-409-995-2	Sequence 2, Appl
29	117.5	5.5	1098	3	US-08-685-467-2	Sequence 2, Appl
30	117.5	5.5	1098	3	US-09-377-155-32	Sequence 32, Appl
31	117.5	5.5	1098	3	US-08-913-942-2	Sequence 2, Appl
32	117.5	5.5	1098	3	US-09-669-974-32	Sequence 32, Appl
33	117.5	5.5	1098	3	US-09-268-347-44	Sequence 44, Appl
34	117.5	5.5	1098	4	US-09-797-862-32	Sequence 32, Appl
35	117.5	5.5	1098	4	US-09-684-707-2	Sequence 2, Appl
36	116.5	5.4	1104	3	US-08-923-992A-4	Sequence 4, Appl
37	115.5	5.4	5024	4	US-09-710-279-2964	Sequence 2964, Ap
38	113.5	5.3	941	3	US-09-074-658-75	Sequence 75, Appl
39	113	5.2	2353	3	US-09-377-155-33	Sequence 33, Appl
40	113	5.2	2353	3	US-08-913-942-4	Sequence 4, Appl
41	113	5.2	2353	3	US-09-669-974-33	Sequence 33, Appl
42	113	5.2	2353	4	US-09-797-862-33	Sequence 33, Appl
43	113	5.2	2353	4	US-09-684-707-4	Sequence 4, Appl
44	113	5.2	2777	4	US-09-543-681A-6124	Sequence 6124, Ap
45	112.5	5.2	1166	4	US-09-200-650E-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-09-182-625F-14
Sequence 14, Application US/09182625F
Patent No. 6506892
GENERAL INFORMATION:
APPLICANT: Bazar, Andrew C.
TITLE OF INVENTION: Polynucleotide Encoding a Mycoplasma Protein Involved in Cell Gr
FILE REFERENCE: BLAZ-101XCI
CURRENT APPLICATION NUMBER: US/09/182,625F
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: US 60/063,701
PRIOR FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 14
LENGTH: 404
TYPE: PRT
ORGANISM: Mycoplasma fermentans
US-09-182-625F-14

Query Match      17.6% Score 378.5; DB 4; Length 404;
Best Local Similarity 26.7%; Pred. No. 3.5e-27;
Matches 115; Conservative 86; Mismatches 156; Indels 71; Gaps 17;

QY      31 NERKSEIIMAAKADANKH-----FGLNMAIVTAGTVNDNSFNQSGWEAI 74
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      3 NNDSENI SPKEDISKVTNNANGQVVKNAELKLPILITDEGKIDKSFNQSAREAL 62

QY      75 QQLGALTGERTSDSSTAELEGYSLSANTKNKVNWLSGFQHDATRTWKIEENOLF 134
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      63 KAIKQGIININWEPSSNESAYNSALSGHKIWIWNGFKHQOSIKQY--IDAHBEL 119

QY      135 TEKNIILIGIDWTDENVITGRYINLTYTEBAGLYANASFLAKFPDPTKSAI 194
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      120 ERNOIKIIGIDF-DIEFEYK--FYSLOFNKESAFPTGTAIASWLEQ--DESKAVVA 173

QY      195 VIGGISPAYTDFIAGYIAGIKAMNLKNSDKTKI--TTDKIEINLGFVDPTSKERLEQ 253
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      174 SPFGGARFPGVTTPEBGFAGKILVYNGH--KSKYIHTSPVKLDSGF-----TAGEKMT 226

QY      254 IAS-----KDKSTILANVAGPITEIPSDIANQNDRIYLGVTDSLVYTKRKN 303
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      227 VINNVLSSTPADVYNPHVILSVAGPAT--FETVRLANKQYVGVSDQGM--QDKDR 282

QY      304 FETSIILKNLGVSFVSVDL-----YTKKSNRNLAGFEFGKSAATVYLGIDRF 353
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      283 ILSVLKHIKQAVETLIDILILEKEBGYKPYVVDKADKWSIFGQ-----KEKW 334

QY      354 VDIADTSLBGNKKL-ATEAISEAKKEFEKTKTTPAEVVRKTLIEIPMPD-KOPDKOE 411
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Query Match	9.5%	Score 204	DB 4	Length 363
Best Local Similarity	25.7%	Pred. No. 9.8e-11		
Matches	98	Conservative	53	Mismatches 147, Indels 84, Gaps 18
Qy	33	RKSEIMAKADANHGFLNMAIVTAGGVNNSFNQSGMEAIQQLGA--LTGGEITVD	89	
Db	38	RSNNMASSSDVK---TKAIVITDTGVDKSFQSGMEGLQMGKKNLSKNGPIYF	93	
Qy	90	SSIALE-----GRYSLANTKNKVVVLSGFQHDADFTRWLKIPIENKQLPTEKNI	140	
Db	94	QSTSEADVANNLQQAAGSYNLI-----FQVGLNHNAYBEAKKHTDNLVY	139	
Qy	141	ILGLDITDTEENVITGGRYINLTYTTEAGMLAGVANNASFLLAKPPSPDPTKSAIVIGGI	200	

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1  COMPUTER:  HP Vectra 486/33
2  OPERATING SYSTEM:  MSDOS version 6.2
3  SOFTWARE:  ASCII text
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER:  US/08/961,083
6  FILING DATE:
7  CLASSIFICATION:  435
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER:
10 FILING DATE:
11 ATTORNEY/AGENT INFORMATION:
12 NAME:  Brookes, A. Anders
13 REGISTRATION NUMBER:  36,373
14 REFERENCE/DOCKET NUMBER:  PB340P2
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE:  (301) 309-8504
17 TELEFAX:  (301) 309-8512
18 INFORMATION FOR SEQ. ID NO.:  8:
19 SEQUENCE CHARACTERISTICS:
20     LENGTH:  328 amino acids
21     TYPE:  amino acid
22     STRANDEDNESS:  single
23     TOPOLOGY:  linear
24 MOLECULE TYPE:  protein
25
26 US-08-961-083-8

```

Query March 9; 4%; Score 202; DB 3; Length 328;
Best Local Similarity 25.7%; Pred. No. 1.3e-10;
Matches 99; Conservative 55; Mismatches 145; Indels 84; Gaps 19

Oy 33 RKSEINAAKADANKHFGILNMAIVTAGTVDNDSFNQSGMEAIQQLG--LITGELITSVD 89
 | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 3 RSRNRNAASSDVK---TKAIVTDYTGVDVKKSFNQSMEDGLQAMGKEHNLSKDNGPTTF 58
 | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Oy 90 STFALE-----GKYSSLATNNKNWVLSTGFQHDATFRLMLKPEHKOLFTENNII 140
 | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :

```

Db      59  QSTSEADYANNLQQAAGSNLIFGV-----GFALNNA-----VKDAAKHTDLNLY 104
Qy      141  ILGIMWTDENYIPFGRIYNLTYYKTEADGMLAGYAANAFLAKKFPBDDPTTKSAIVIGGGI 200
Db      105  LIDVVIKQKN-----ASVTFADNESGYLGVAAAK-----TTKTKGVFVGGI 149
Qy      201  -SPAVTDFIAGYIAGIKAWNLRKNSDKTYITTDKIEINLGFVDVDTSTYERLEIQAISKDK 259
Db      150  ESEVISRFBAEGFKAGV-----ASVDSPIKQVDDYAG-SFG-DAAKGTITAAQYAAAGAD- 201
Qy      260  PSTLLAVAGPL-TEIFSDLIANQNR-----YLIEVDPDQSL-VYT---KTKAKFF 306
Db      202  --IVYQVAGGTGAGVFAEAKSLNESBPENEKQWAVIGVDDQEAEGKTYISKQESNFWLV 259
Qy      307  SILKNIAGYVSPFVSLDLYTKKSNRNRIAGFEFGKSAATVYLGIKDRFVDIADTSLBENDK 366
Db      260  STLKQVGTVKDI-----SNKARBGSPGGQ--VIVYSLKDGVDLAVTNLSBEK 308
Qy      367  KLATEAISEAKKFEBEKTTIP 388
Db      309  K---AVEDAKAKIIDGSVKVP 326

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```

1      RESULT 7
2      US-09-536-784-8
3      ; Sequence 8, Application US/09536784
4      ; Patent No. 6573082
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Choi et. al.
7      ; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
8      ; NUMBER OF SEQUENCES: 452
9      ; CORRESPONDENCE ADDRESS:
10     ; ADDRESSEE: Human Genome Sciences, Inc.
11     ; STREET: 9410 Key West Avenue
12     ; CITY: Rockville
13     ; STATE: Maryland
14     ; COUNTRY: USA
15     ; ZIP: 20850
16     ; COMPUTER READABLE FORM:
17     ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
18     ; COMPUTER: HP Vectra 486/33
19     ; OPERATING SYSTEM: MSDOS version 6.2
20     ; SOFTWARE: ASCII Text
21     ; CURRENT APPLICATION DATA:
22     ; APPLICATION NUMBER: US/09/536,784
23     ; FILING DATE: 30-Oct-1997
24     ; CLASSIFICATION: <Unknown>
25     ; PRIOR APPLICATION DATA:
26     ; APPLICATION NUMBER: 08/961,083
27     ; FILING DATE: OCT-30-1997
28     ; ATTORNEY/AGENT INFORMATION:
29     ; NAME: Michelle S. Marks
30     ; REGISTRATION NUMBER: 41,971
31     ; REFERENCE/DOCKET NUMBER: PB340P3
32     ; TELECOMMUNICATION INFORMATION:
33     ; TELEPHONE: (301) 309-8504
34     ; TELEFAX: (301) 309-8512
35     ; INFORMATION FOR SEQ ID NO: 8:
36     ; SEQUENCE CHARACTERISTICS:
37     ; LENGTH: 328 amino acids
38     ; TYPE: amino acid
39     ; STRANDEDNESS: single
40     ; TOPOLOGY: linear
41     ; MOLECULE TYPE: protein
42     ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
43     ; US-09-536-784-8

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Query Match          9 4%; Score 202; DB 4; Length 328;
Beet Local Similarity 25.7%; Pred. No. 1.3e-10;
Matches 98; Conservative 55; Mismatches 145; Indels 84; Gaps 19;
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[illegible]

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1      RESULT 8
2      US-09-107-532A-5084
3      Sequence 5084, Application US/09107532A
4      Patent No. 6583275
5      GENERAL INFORMATION:
6      APPLICANT: Lynn A Doucette-Stamm and David Bush
7      TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
8      ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
9      NUMBER OF SEQUENCES: 7310
10     CORRESPONDENCE ADDRESS:
11     ADDRESSEE: GENOME THERAPEUTICS CORPORATION
12     STREET: 100 Beaver Street
13     CITY: Waltham
14     STATE: Massachusetts
15     COUNTRY: USA
16     ZIP: 02354
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: CD-ROM ISO9660
19     COMPUTER: PC
20     OPERATING SYSTEM: <Unknown>
21     SOFTWARE: ASCII
22     CURRENT APPLICATION DATA:
23     APPLICATION NUMBER: US/09/107,532A
24     FILING DATE: 30-Jun-1998
25     PRIOR APPLICATION DATA:
26     APPLICATION NUMBER: 60/085,598
27     FILING DATE: 14 May 1998
28     APPLICATION NUMBER: 60/051571
29     FILING DATE: July 2, 1997
30     ATTORNEY/AGENT INFORMATION:
31     NAME: Arinello, Pamela Deneka
32     REGISTRATION NUMBER: 40,489
33     REFERENCE/DOCKET NUMBER: GTC-012
34     TELECOMMUNICATION INFORMATION:
35     TELEPHONE: (781)893-5007
36     TELEFAX: (781)893-8277
37     INFORMATION FOR SEQ. ID NO: 5084:
38     SEQUENCE CHARACTERISTICS:
39     LENGTH: 374 amino acids
40     TYPE: amino acid
41     TOPOLOGY: linear
42     MOLECULE TYPE: Protein
43     HYPOTHEetical: YES
44     ORIGINAL SOURCE:
45     ORGANISM: Enterococcus faecium
46     FEATURE:
47

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NAME/KEY: misc.feature
LOCATION: (B) LOCATION 1...374
SEQUENCE DESCRIPTION: SEQ ID NO: 5084:
US-09-107-532A-5084

Query Match 9.4%; Score 202; DB 4; Length 374;
Best Local Similarity 25.2%; Pred. No. 1.6e-10;
Matches 95; Conservative 63; Mismatches 133; Indels 86; Gaps 19;

QY AIYTAGTVDNDSNOSGWEAIOQLGALTGEITSVSSSTAELEGKXSSILANTKNVW- 111
DB ALITDVGVDNRSPNOSAMEGLEKMK- - - - -DQGSRGNDGFQYRQSSNESDYIP 108
QY 112 - - - - -LSGFQ--HGDAFTWMLKIPENKQLFTENKIIILG--IDWTDENVIPGRYINL 161
DB 109 NIOQALNAGKFTIGIGYKLPKPAEQATNNTGTFPIIDVIDGLD--NV- - - - -VSA 160
QY 162 TYTEAGWLAGYANASFLAKKPSDPTKSAIVIGGISPATVD-PIAGYLAKIKAMNL 220
DB 161 TPKDNEASVLAGVAAAY- - - - -TTENVVGFIGGVKGEVIDRFDAGKAGVDA-GA 210
QY 221 KNSDKTKITTDKEINLGFVDVDTSTKERLEQIA- - - - -SKDKSTLLAAGPLTELISD 276
DB 211 KEJGKEIKV- - - - -LNOYAGDSAPDGRSIAQGMVQNMADIIFHAGSGTGNVFOE 262
QY 277 I--IANONDR--YLIGVDTDS- - - - -LVYTKTKNKKFFTSILKULGYSVFSVLSDLTYTK 327
DB 263 AKSLNEDGDKKVVIGVDRQSDSGEYTLNGEKKNFLLSTLKVAG- - - - -TVEDDLAOKS 318
QY 328 SNSRNLAGFEFGKSAATVYIGIKRFDVADIADTSLEGNKKLATEAISEAKKEFEKTKTI 387
DB 319 ADGK- - - - -FPGGEHTVY-GLKEDGVGLTEGQLSDEAKK- - - - -AVDEAKEKI- - - - - 360
QY 388 PAEEVKTEIPEMPDK 404
DB 361 - - - - -ISGDVAKVPEETPEE 373

RESULT 9

US-09-071-035-80
Sequence 80, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071.035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-80

Query Match 8.3%; Score 178; DB 4; Length 339;
Best Local Similarity 25.1%; Pred. No. 2.5e-08;
Matches 103; Conservative 51; Mismatches 140; Indels 116; Gaps 20;

QY 33 RKEIIMAAKADANKHFGLNMAIVTAGTVDNDSFNOSGWEAIOQLGA--LTGGE- - - - - 84
DB 7 KTAESGGGKDA- - - - -ASHAVIITDTCGVDDKSFNOSWEGLOAWGKEHDLPEGSKGAY 62
QY 85 ITSVDSS--TAELEGKSSILANTKNVWVLSGFQHGAFRMLKIPENKQLFTENKIIIL 142
DB 63 IQSNDADYTTNIDQAVSSKEFTIFGI- - - - -GYLLKDA- - - - -ISSAADANPDTNFVLI 112
QY 143 GIDWTDENVIPGRYINLTYTEAGWLAGYANASFLAKKPSDPTKSAIVIGGISP 202
DB 113 DDQIDGKAV- - - - -VSATFRDNEAAYLAGVAAA- - - - -NETKTKNKGVSGBEG 157
QY 203 AVTD-PIAGYLAKIKAMNLKNSDKTKITTDKEINLGFVDVDTSTKERLEQIASDKPS 261
DB 158 VVIDRFOAGFEKGV-ADAKELEKEITVDT- - - - -KYAASFADPA 196
QY 262 TLLAVAGPLTEIFSDIT- - - - -ANONDR-YLIGVDTDSL--VYT 298
DB 197 KGRALAAAMYQNGVDIIFHAGSGATGCGFQEARDLNDSGGDKRWVIGVDRDADGKY- 255
QY 299 KTK- - - - -NKEFTSILKULGYSVFSVLSDLTYTKSNSRNLAGFEFGKSAATVYIGIKRDF 353
DB 256 KTKDGEKDNFTLSTLKGVTAVODIANRLBCK- - - - -FPGGEHLVY-GLDDCG 304
QY 354 VDIADTSLEGNKKLATEAISEAKKEFEKTKTIPEAEVKTEIPEMPD 403
DB 305 VDLTDGYL--NDKT- - - - -KEAVTKAKDKVISGDVAVPEKPE 339

RESULT 10

US-08-396-957A-5
Sequence 5, Application US/08396957A
Patent No. 5780041
GENERAL INFORMATION:
APPLICANT: SIMPSON, WARREN, SCHWAB, TOM G.
TITLE OF INVENTION: ANTIGENIC PROTEINS AND
TITLE OF INVENTION: GENES ENCODING SAME OF BORRELIA BURGDOFFERI.
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396.957A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/020,245
FILING DATE: 19-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/664,731
FILING DATE: 05-MAY-1991

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;
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: 07/487,716
; FILING DATE: 05-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4018054
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 341
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Borrelia burgdorferi
; STRAIN: Sh-2-82
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; FEATURE:
; NAME/KEY: p39a
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: p39a protein sequence
;
US-08-396-957A-5

Query Match      8.3%; Score 178; DB 1; Length 341;
Best Local Similarity 26.9%; Pred. No. 2.5e-08;
Matches 101; Conservative 58; Mismatches 124; Indels 92; Gaps 25;

QY 44 ANKHFGIMAVITAGTVNDNSFNQSGWEAIIQOLGALGSEITVSSTAELEGKYS-- 101
DB 24 SSKKIKISMV--DGVLDKSFNSANEALLRLKQDPENIEEYFS--CAISGYSSSYV 78
QY 102 --LAANTKN--VWVLSGFQHGDAFTRWLKI PENKQLFTEKNII--ILGIDWTDTEENVI 153
DB 79 SDLNLKRNQSDLIW-LVGYMLTDA--SLVSSSEPKI--SYGIIDPIYGDVQIPEMLI 133
QY 154 PTGRYINLTYTEAGWLAGY--ANASFLAKKFPSPDPTKRSATYIG--GGISPAVTD-FI 208
DB 134 A-----VVFVEGAGFLAGYIAAKKSPSGK-----IGFIGMKGNIVDAFR 174
QY 209 AGYLAGIKAWNLKNSDKTKITTDKIEINLGFVDVDTSTKERLQIASK--DKPSTLLAV 266
DB 175 YGYSAGAKYAN-KDIEIISSEVNSGSPVDIG-----RTIASKMYSKIGDIVIH 221
QY 267 AGPLTEI-FSDIIANOND-RYLIGVDTQSLVYTKRKPFSTILKNLGYSVFSLDLY 324
DB 222 AAGLAGIGVIAAANLGDGYVVIIGADQOS--YLAPEK-FITSVIKNIGDALYILTGE-Y 277
QY 325 TKKNSRLAGFEPGKKSATYILGIKDFVIADITSLSEGNKDLATEISAKKEFEKKT 384
DB 278 IKNNNV-----WEGGK--VVQMGIRDGVIGLIPNAN-----EF-EYI 310
QY 385 KTI PAEVRKTLBIP 399
DB 311 KVLERKIVNKEIIVP 325

RESULT 11
US-09-071-035-78
; Sequence 78; Application US/09071035
; Patent No. 6448043
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; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brooker
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-071-035-78

Query Match      8.3%; Score 178; DB 4; Length 361;
Best Local Similarity 25.1%; Pred. No. 2.8e-08;
Matches 103; Conservative 51; Mismatches 140; Indels 116; Gaps 20;

QY 33 RKSEIMAAKADANKHFGIMAVITAGTVNDNSFNQSGWEAIIQOLGA--LTGSE----- 84
DB 29 KTAESGGGKGD-----AHSAVIITDTGVDKSFNSQSGWGLQMGKEHDLPEGSKGYAY 84
QY 85 ITSVDS--TAELGKYSLSLANTKNVWVLSGFQHGDAFTRWLKI PENKQLFTEKNIIIL 142
DB 85 IQSNDADVYTNIDQAVSSKFNITFGI--GYLLKDA-----ISSAADANPDTNVL 134
QY 143 GIDWTDTEENVIPTGRYINLTYTEAGWLAGYANASFLAKKFPSPDPTKRSATYIGGISP 202
DB 135 DDQIDGKKNV-----VSATPFRODEAAYLAGVAAA-----NETKTNKVGVGEBG 179
QY 203 AVTD-PIAGYLAGIKAWNLKNSDKTKITTDKIEINLGFVDVDTSTKERLQIASKKPS 261
DB 180 VVIDRFQAGFEKGV-ADAARELKEITVDT-----KYAASFADPA 218
QY 262 TLAAVAPLRIEIPSDII-----ANQNR-XLIGVDTQSL--VYT 298
DB 219 KGRKLAAMQONGVDIIFHASGATGQVFOEAKDLNMSGGDKWVIGVDRDQADGKY- 277
QY 299 KTK-----NKEFTSILKNLGYSVFSLDLYTKKNSRNLAGFEFGKKSATVYLGIDRF 353
DB 278 KTDGKEDNFTLSTLKGAVGTAVDIANRLBCK-----FPGGELHYV-GLMDGG 326
QY 354 VDIADTSLSEGNKDLATEISAKKEFEKKTITIPAEVRKTLBIPMPD 403
DB 327 VDLTDGYL--NDKT-----KEAVKTAQDKVIGDVVPEKPE 361

RESULT 12
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US-09-134-000C-6005
 ; Sequence 6005, Application US/09134000C
 ; Patent No. 6617156
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134,000C
 ; PRIOR FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6005
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Enterococcus faecalis
 ; US-09-134-000C-6005

Query Match 8.3%; Score 178; DB 4; Length 375;
 Best Local Similarity 25.1%; Pred. No. 3e-08;
 Matches 103; Conservative 51; Mismatches 140; Indels 116; Gaps 20;

QY 33 RKSEIMAKADANKHFGIINAVITAGGTVDNDSFNQSGWEALIQOLGA---LTGGE-----84
 DB 43 KTAESGGGKGA---AHSAVIITDGTGVDKSFNQSWEGLQWKGKHDLPESKGYAY 98
 QY 85 ITVDSS--TAELEGKSSLANTKNVVLSGFQHGAFTRMLKIPENKQLPENKIIIL 142
 DB 99 IQSNDADYTNIDQAVSSKFNITFGI---GYLLKPA-----ISSADANPPTNVL 148
 QY 143 GIDMTDENVYIPGRVYNLTYTEBAGMLAGYANASFLAKKPSDPKRSATVIGGISP 202
 DB 149 DDQIDGKNV-----VSATFRDNEAAYLVGVA---NEFTKNVGVGSEEG 193
 QY 203 AVTD-PIAGYLAGIKAWNLKNSDKKITTTDKIEINLGFVDVDTSTKERLEQIASKDKPS 261
 DB 194 VVIDRFGAGFEKGV-ADAALGLEITVDI-----KYAASFADPA 232
 QY 262 TLAAVAGPLTEISDII-----ANONDR-YLIGVDTDSL-VYT 298
 DB 233 KGAALAAWYQNGVDIIFHAGATGCGVFOEAKDLNDSGSGDKWVIGVDRDQADGKY- 291
 QY 299 KTK-----NKFSTILKNLGYSVFSVSDLYTKKSNRNLAGFEFGKKSATVYIGIDRF 353
 DB 292 KTKDGEDNFTLTSTLKGVTAVODIANRLDEK-----FPGGEHLVY-GLKDG 340
 QY 354 VDIADTSLGNDKRLATEAISEAKKEFEKTKTIPAEVVKTLIEIPMPD 403
 DB 341 VDLTDGVL--NDKT-----KEAVKTKAKDVIGSDVAVPEKPE 375

RESULT 13
 ; US-09-134-000C-6004
 ; Sequence 6004, Application US/09134000C
 ; Patent No. 6617156
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134,000C
 ; PRIOR FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6004
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: Enterococcus faecalis
 ; US-09-134-000C-6004

Query Match 8.1%; Score 174; DB 4; Length 362;
 Best Local Similarity 24.1%; Pred. No. 6.7e-08;
 Matches 96; Conservative 67; Mismatches 132; Indels 104; Gaps 20;

QY 40 AKADAN-----KFGIINAVITAGGTVDNDSFNQSGWEALIQOLGALTGEITSVDSSTAS 94
 DB 32 SKKNATKDPQH---SVWVITDGTGIDKSFNQSWEGLQWKGKHDLPESKGYAY 86
 QY 95 LEKYSGLANTKNQWVLSGFG--HGDAPFRMLKIPENKQLPENKIIIGIDMTDENV 152
 DB 87 IQSNEASDYSNTIDQAVSSQKTFIIGYLLKNAVDADANPPTNVL---DPTVN- 141
 QY 153 IPTGRVYNLTYTEBAGMLAGYANASFLAKKPSDPKRSATVIGGISPAVDTPIAGY 211
 DB 142 -GKNNAASATFRNESAIVLAGVAA-----NFTKNVGFIVGSEVPIGRFAGF 191
 QY 212 LAGIKAWNLKNSDKKITTTDKIEINLGFVDVDTSTKERLEQIASDKPESTLAAVAPLT 271
 DB 192 EKGV-----ADAGK-----LGKDIQITSTVAGTFADASKR-----ALASMY 230
 QY 272 EIFSII-----ANONDRYLIGVDTDSL-VYT-----KTGKF 304
 DB 231 QAGADIIYHAAATGCGIFOEAKALNETGSKDRVWVIGVDRDQEDGKTTKDGKDNLT 290
 QY 305 FTSILKNLGYSVFSVSDLYTKKSNRNLAGFEFGKKSATVYIGIDRPIADTSLG 364
 DB 291 LASTIGVNIIV-KKISDLALDEK-----FPGGEH---LTYGLKDGVD-----330
 QY 365 DKXLATEAIS-EAKKEFEKTKTIPAEVVKTLIEIPMPD 402
 DB 331 -LTFEALSDQAKTAVKEAKEQIISGDVK---VPDQ 362

RESULT 14
 ; US-09-182-625F-6
 ; Sequence 6, Application US/09182625F
 ; Patent No. 6506892
 ; GENERAL INFORMATION:
 ; APPLICANT: Webb, Andrew C.
 ; APPLICANT: Blazar, Beverly A.
 ; TITLE OF INVENTION: Polynucleotides Encoding a Mycoplasma Protein Involved in Cell Gtr
 ; FILE REFERENCE: BLAZ-101XCI
 ; CURRENT APPLICATION NUMBER: US/09/182,625F
 ; PRIOR FILING DATE: 1998-10-29
 ; PRIOR APPLICATION NUMBER: US 60/063,701
 ; PRIOR FILING DATE: 1997-10-29
 ; NUMBER OF SEQ ID NOS: 16
 ; SEQ ID NO 6
 ; LENGTH: 166
 ; TYPE: PRT
 ; ORGANISM: Mycoplasma fermentans
 ; FEATURE:
 ; OTHER INFORMATION: Peptide
 ; US-09-182-625F-6

Query Match 8.0%; Score 173; DB 4; Length 166;
 Best Local Similarity 27.3%; Pred. No. 2.4e-08;
 Matches 50; Conservative 37; Mismatches 56; Indels 40; Gaps 8;

QY 197 GGGISPAVTFPIAGYLAGIKAWNLKNSDKKITTTDKIEINLGFVDVDTSTKERLEQIA 255
 DB 2 GCGAFPGVTFPIAGYLAGIKAWNLKNSDKKITTTDKIEINLGFVDVDTSTKERLEQIA 255
 QY 256 S-----KDPSTLAAVAPLTETESDIIANONDRYLIGVDTDSL-VYTKKNKFF 305
 DB 55 NNVLSTPADVKNPFIYILSVAGPAT--FEFTVLANKGQYIVDSQGM--QDKRIL 110
 QY 306 TSLIKNLGYSVFSVLSL-----YTKKSNRNLAGFEFGKKSATVYIGIKDRFVD 355
 DB 111 TSVLKHITQAVETTLDDLLEKEBGKPYVVKAKKADKMSHFQTO-----KEKMG 162

QY	356	IAD	358
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Db	163	VAE	165

RESULT 15

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US-08-396-957A-4
Sequence 4, Application US/08396957A
Patent No. 5780041
GENERAL INFORMATION:
APPLICANT: SIMPSON, WARREN, SCHWAN, TOM G.
TITLE OF INVENTION: ANTIGENIC PROTEINS AND
TITLE OF INVENTION: GENES ENCODING SAME OF BORRELLIA BURGDORFERI.
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,957A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 435
FILING DATE: 08/020,245
FILING DATE: 19-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 435
FILING DATE: 07/664,731
FILING DATE: 05-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,716
FILING DATE: 05-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4018U54
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 339
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Borrelia burgdorferi
STRAIN: Sh-2-82
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY: p39'
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: p39', protein
OTHER INFORMATION: sequence.
US-08-396-957A-4

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2004, 01:26:40 ; Search time 97.7643 Seconds
(without alignments)
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Title: US-09-676-249D-4

Perfect score: 2155
Sequence: 1 MMDETTEKESADNQNKQI.....KOPDKQESIDKLTIDINNL 423

Scoring table: BLOSUM62
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Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220.5	10.2	350	US-10-474-792-166	Sequence 166, Appl
2	216.5	10.0	330	US-10-451-337-12	Sequence 12, Appl
3	216.5	10.0	330	US-10-451-337-14	Sequence 14, Appl
4	216.5	10.0	330	US-10-451-337-39	Sequence 39, Appl
5	216.5	10.0	330	US-10-451-337-40	Sequence 40, Appl
6	216.5	10.0	330	US-10-451-337-41	Sequence 41, Appl
7	213.5	9.9	330	US-10-451-337-16	Sequence 16, Appl
8	213.5	9.9	330	US-10-451-337-42	Sequence 42, Appl
9	209	9.7	344	US-10-451-337-6	Sequence 6, Appl
10	202	9.4	328	US-09-765-272-8	Sequence 8, Appl
11	202	9.4	350	US-09-769-787-132	Sequence 132, Appl
12	178	8.3	339	US-09-071-035-80	Sequence 80, Appl
13	178	8.3	339	US-10-206-576-80	Sequence 80, Appl

14	178	8.3	361	US-09-071-035-78	Sequence 78, Appl
15	178	8.3	361	US-10-206-576-78	Sequence 78, Appl
16	174	8.1	347	US-10-451-337-8	Sequence 8, Appl
17	174	8.1	347	US-10-474-792-180	Sequence 180, Appl
18	173	8.0	356	US-09-760-541-6	Sequence 6, Appl
19	168	7.8	357	US-10-282-122A-60484	Sequence 60484, A
20	151.5	7.0	223	US-09-769-736-48	Sequence 48, Appl
21	148	6.9	797	US-10-156-761-10907	Sequence 10907, A
22	137.5	6.4	889	US-09-952-267-15	Sequence 15, Appl
23	133.5	6.2	1786	US-09-742-096-3	Sequence 3, Appl
24	133.5	6.2	1787	US-10-415-253-2	Sequence 2, Appl
25	127.5	5.9	496	US-10-451-467A-432	Sequence 432, App
26	127	5.9	2045	US-10-282-122A-74463	Sequence 74463, A
27	127	5.9	2059	US-10-474-792-62	Sequence 62, Appl
28	124.5	5.8	998	US-10-282-122A-70450	Sequence 70450, A
29	121.5	5.6	1073	US-10-193-764-45	Sequence 45, Appl
30	121.5	5.6	1079	US-10-193-764-43	Sequence 43, Appl
31	121.5	5.6	1849	US-10-637-544-2	Sequence 2, Appl
32	121	5.6	852	US-10-282-122A-62892	Sequence 62892, A
33	121	5.6	902	US-10-437-963-105564	Sequence 105564, A
34	120.5	5.6	2457	US-10-282-122A-49854	Sequence 49854, A
35	120	5.6	1946	US-10-282-122A-62947	Sequence 62947, A
36	119	5.5	2285	US-09-932-183A-2	Sequence 2, Appl
37	118.5	5.5	1963	US-10-282-122A-73978	Sequence 73978, A
38	118.5	5.5	6641	US-10-282-122A-70580	Sequence 70580, A
39	118.5	5.5	10203	US-10-661-809-23	Sequence 23, Appl
40	118	5.5	1031	US-10-282-122A-54611	Sequence 54611, A
41	117.5	5.5	392	US-10-194-489-22	Sequence 22, Appl
42	117.5	5.5	719	US-10-239-610-2	Sequence 2, Appl
43	117.5	5.5	1098	US-09-797-862-32	Sequence 32, Appl
44	116.5	5.4	571	US-10-282-122A-53248	Sequence 53248, A
45	116.5	5.4	1104	US-09-797-385-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-10-474-792-166
Sequence 166, Application US/10474792
Publication No. US20040236072A1
GENERAL INFORMATION:
APPLICANT: Olmsted, Stephen
APPLICANT: Zagursky, Robert
APPLICANT: Nickbarg, Elliot
TITLE OR INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
FILE REFERENCE: AM 100399
CURRENT APPLICATION NUMBER: US/10/474, 792
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 674
SOFTWARE: PatentIn version 3.0
SEQ ID NO 166
LENGTH: 350
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-10-474-792-166

Query Match 10.2%; Score 220.5; DB 17; Length 350;
Best Local Similarity 27.8%; Pred. No. 2.6e-08;
Matches 103; Conservative 49; Mismatches 150; Indels 69; Gaps 17;
QY 39 AAKADAKHFGIMNAIVTAGTVNDSFNOSGMAIQOLGALNS-GEITSVDSSTAELEG 97
DB 26 ASKAGASGCKTDLKVAMVTDGTGVDKSFNOSAMEGLSKWKGMLQKGTGEDYQSTSES 85
QY 98 KYSSLANTNNKXVWVLTSGFO--HGDAFTRMUKIPENKOLFTFKNIILIGIDMTDENVIPT 155
DB 86 EVA-----TNDLTAVNSGVYQILYIGIFA--LKDAIAKAAGNDEGVKFTIID---DIEGK 135
QY 156 GRYINLTYKTEBEAGMLAGYANASFLAKFPSDPKRSALV-VIGGISPATYDFAVLG 214
DB 136 DNVAIVTFADHEAAYIAGIAAK-----TTKTYGVGVGMEGTVITRFEKGFAG 186

```

QY 215 KANWLNKSDKKTKTITTDKIEINLGE-----DVQDSTHERLEQIASKOKSPILLAVAGE 269
Db 187 VKS-----VDDTIOVKVDYAGSFGDAKGMTIAAOYAAGAD-VIYOAGGT 232
QY 270 LTELPSDIANONDR-----YLIGVDITQO--SLVYT-----KTKNKFPTSILNLSYSVE 317
Db 223 GAGVNEAKAINERKSEADKWAVIGVDRQOKEGKTTSDGKEANVVLASSITEVGRVQ 292
QY 318 SVLSDLTYRKKSNSRNLAGFEGGKATVYLGIKDFVADIADTSLBGNDDKLATEAISEAK 377
Db 293 LINKOVADKK-----FPGGK--TIVY-GLKDGVEIATY---NVSKEAVKAIKEAK 337
QY 378 KEFEKTKTIP 388
Db 338 AKIKSGDIKVP 348

```

```

RESULT 2
US-10-451-337-12
Sequence 12, Application US/10451337
Publication No. US20040097706A1
GENERAL INFORMATION:
APPLICANT: SHIRE BIOCHEM INC.
APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard R.
APPLICANT: HAMEL, Josee
APPLICANT: RIOUX, Stephanie
APPLICANT: RHEAULT, Patrick
TITLE OF INVENTION: STEPHINOCOCCUS PYOGENES ANTIGENS AND
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 12806-24PCT
CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 330
TYPE: PRT
ORGANISM: S. pyogenes
US-10-451-337-12

```

Query Match	10.0%;	Score 216.5;	DB 15;	Length 330;
Best Local Similarity	28.3%;	Pred. No. 4,7e-08;		
Matches 102; Conservative	46;	Mismatches 143;	Indels 69;	Gaps 17;

Qy 39 AAKADANRHPGLNMMILVTFAGTGVNDSPFQSGEALQOQALG--GEITSVDSSTLEEG 97
 Db 19 ASKGAQSGKTDLKAVMAMVTDGSGVDDKSPFQSGAMEGLOSGKMGLOKQGFDFQSGSTSES 78
 Qy 98 KYSSILANNNKAVWVLVSGFQ--HGDAFTRLMKLPENKQLFTEKNIITLIGIDMTDENTVILPT 155
 Db 79 EYA-----TNLDPAVSGGYOLIVGIGPA--LKQAIAPAGADNBEKRVKIID---DIEEGK 128
 Qy 156 GRYNLITKTEEPAGMLAGVANAFLAKRFPSPDTRKSAI--VIGGGISPAVTFEITAGVLG 214
 Db 129 DNVAQSVTFADHHAALVAGIAA--TTTKTKYVFGVQSGMGTYITREKFEAG 179
 Qy 215 IKANMLKNSDKKTKITTTDKIEINLGF---DVQDTSTYERLEQIASKQKPSLLAVAGP 269
 Db 180 VKS-----VDDTIQVKVAVAGSGFGAANKGTIAAQAAGAD--VITYAAGGT 225
 Qy 270 LTEIFSDIIANONDR-----YLIGVDTPQ--SLVYT-----KTKNKFPTSILKNLGVSYE 317
 Db 226 GAGVFNEMAKAIIEKRSSEADKXWAVIGVDPRQDQBEKGTISDQGEANVLAASSIKVEYKAVQ 285
 Qy 318 SVLSDLITKKSNSRLNLAGFEPFGKGSATVYLGIKDRFVIDIADTSLBQNDKKLATEAISEAK 377
 Db 286 LIRKQVADKK-----FPGGK--TTVY-GKDGGEVETALT---NVSKEAVKALAEAK 330

```

RESULT 3
US-10-451-337-14
; Sequence 14, Application US/10451337
; Publication No. US20040097706A1
; GENERAL INFORMATION:
; APPLICANT: SHIRE BIOCHEM INC.
; APPLICANT: MARTIN, Denis
; APPLICANT: BRODEUR, Bernard R.
; APPLICANT: HAMEL, Josee
; APPLICANT: RIOUX, Stephane
; APPLICANT: RHEAULT, Patrick
; TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS AND
; TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
; FILE REFERENCE: 12806-24PCT
; CURRENT APPLICATION NUMBER: US/10/451.337
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: US 60/256,940
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 330
; TYPE: PR1
; ORGANISM: S. pyogenes
US-10-451-337-14

```

Query Match	10.0%;	Score 216.5;	DB 15,	Length 330;
Best Local Similarity	28.3%;	Pred. No. 4.7e-08;		
Matches 102;	Conservative 46;	Mismatches 143;	Indels 69;	Gaps 17;

```

Oy      39  AAKKDANHGFIENMAIYVAGGTVDNDSNFOGMEWAIQOLGALYT-GEITSVDSSTLELG  97
Db      19  ASKGSAGSCKTDLYKAMVITDTGSGVDKSNFQSGAMBELQSGKMGELQKGTGFDFYFGSTSS  78

Oy      98  KYSSLANTNNKVVWVLSGFQ--HGDAFTWMLKPEKKQLETEKNIIILGIDMTDTEVIT  155
Db      79  EYA--"TNDTAVAGSGYQLIYGIGA--LKDALAKAAGDNNGVAFVIID---DILEEK  128

Oy      156  GRVINYLTYTEEAGWLAGVANASFLAKKFPSPDPTKRSAI-VGGGIGISPWDTFIAGLYAG  214
Db      129  DNVASVTFPADHEAAYLAGIAAAK-----TTTKTKIVGFQGMGEVITITPEKGFBAQ  179

Oy      215  IKANNLKNKSDKTKYKITTDKIEINLGF---DVQDSTKERLEQJLASHDKPSTLLAVALP  269
Db      180  VKS-----VDDTIQVKVDYAGSGFGDPAAKGKTTIAAQVYAAGAV--VIQYAGGI  225

Oy      270  LTEIFSDIIANQNDR-----YLIGVPTDQ--SLVYT--KTKNKKFTPSILKNLGSYVF  317
Db      226  GAGVFNEEKAINEKRSSEADKYWVIGVDBDQXQDEKGYTSSKDGKEANPVLASSIKEVGKAVQ  285

Oy      318  SVLSDLTYTKKSNRNLAFGEFGKGSATYYLIGKDFVVIDIADPISLSEGNDDKALATEAISEK  377
Db      286  LNKQVADK-----FPGGK--TTVY-GIKDQGVELAIT---NNSKEAVKALKEKK  330

```

RESULT 4
US-10-451-337-39
Sequence 39 Application US/10451337
Publication No. US20040097706A1
GENERAL INFORMATION:
APPLICANT: SHIRE BIOCHEM INC.
APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard R.
APPLICANT: HAMEL, Josee
APPLICANT: RIOUX, Stephanie
APPLICANT: REHAULT, Patrick
TITLE OR INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS AND
TITLE OR INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 12806-24PPT
CURRENT APPLICATION NUMBER: US/10/451.337
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR FILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 42
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 39
 LENGTH: 330
 TYPE: PRN
 ORGANISM: S. pyogenes
 US-10-451-337-39

Query Match 10.0%; Score 216.5; DB 15; Length 330;
 Best Local Similarity 28.3%; Pred. No. 4.7e-08;
 Matches 102; Conservative 46; Mismatches 143; Indels 69; Gaps 17;

QY 39 AAKADANKHFGMLNAIYTAGTVNDNSFNOSGMEALIQOLGALTG-GEITSVDSSTAIEG 97
 DB 19 ASKGAAGKTDLKVAMVTDGVDKSPNOSAMEGLQSKGEMGLQKGTGDFYQSTSES 78
 QY 98 KYSLANTNNKVVVLSGFQ--HGDAFTRWLKIPEKNKILIGIDMTDTEVNIPT 155
 DB 79 EYA-----TNDTAVSGGYQLYIGIGA--LKDAIAKAGNDEGVKVIID----DIEGK 128
 QY 156 GRVINTLYKTEBAGMLAGVNASFLAKKPSDPTKRSAL-VIGGISPATVDTPIAGYIAG 214
 DB 129 DNVAATVPADHEAAYLAGIAAK-----TTKTTGVPVGMGEGTVITREKGEAG 179
 QY 215 IKAWNLKNSDKKITTDDKIEINLGF----DVODSTKERLEQIASKDKPSTLLAVAGP 269
 DB 180 VKS-----VDDTIGVKVDYAGSFGDAKAGKTIAAQAAGAD--VIYQAAGGT 225
 QY 270 LTFEFSITIANQDR-----YLIQVDTDQ--SLVYT---KTKNKFSTILKNLGYSVF 317
 DB 226 GAGVFNEAKAINEKRSADKRWVIGVDRDQDEGKYSKDGKCANFVLASSIKEVGKAVQ 285
 QY 318 SVLSDLTYTKKSNRNLAGFEFGKKSATVYIGIKDRFVDIADTSLBGNDKLATEAISEAK 377
 DB 286 LINKQVADK-----FPGK--TTVY-GLKDGVEIATY---NVSKEAVKAIKEAK 330

RESULT 5 US-10-451-337-40

Sequence 40, Application US/10451337
 Publication No. US20040097706A1
 GENERAL INFORMATION:
 APPLICANT: SHIRE BIOCHEM INC.
 APPLICANT: MARTIN, Denis
 APPLICANT: BRODEUR, Bernard R.
 APPLICANT: HAMEL, Josee
 APPLICANT: RIOUX, Stephane
 APPLICANT: RHEAULT, Patrick
 TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS AND
 TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
 FILE REFERENCE: 12806-24PCT
 CURRENT APPLICATION NUMBER: US/10/451,337
 CURRENT FILING DATE: 2003-11-18
 PRIOR APPLICATION NUMBER: US 60/256,940
 NUMBER OF SEQ ID NOS: 42
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 40
 LENGTH: 330
 TYPE: PRN
 ORGANISM: S. pyogenes
 US-10-451-337-40

Query Match 10.0%; Score 216.5; DB 15; Length 330;
 Best Local Similarity 28.3%; Pred. No. 4.7e-08;
 Matches 102; Conservative 46; Mismatches 143; Indels 69; Gaps 17;

QY 39 AAKADANKHFGMLNAIYTAGTVNDNSFNOSGMEALIQOLGALTG-GEITSVDSSTAIEG 97
 DB 19 ASKGAAGKTDLKVAMVTDGVDKSPNOSAMEGLQSKGEMGLQKGTGDFYQSTSES 78
 QY 98 KYSLANTNNKVVVLSGFQ--HGDAFTRWLKIPEKNKILIGIDMTDTEVNIPT 155

DB 79 EYA-----TNDTAVSGGYQLYIGIGA--LKDAIAKAGNDEGVKVIID----DIEGK 128
 QY 156 GRVINTLYKTEBAGMLAGVNASFLAKKPSDPTKRSAL-VIGGISPATVDTPIAGYIAG 214
 DB 129 DNVAATVPADHEAAYLAGIAAK-----TTKTTGVPVGMGEGTVITREKGEAG 179
 QY 215 IKAWNLKNSDKKITTDDKIEINLGF----DVODSTKERLEQIASKDKPSTLLAVAGP 269
 DB 180 VKS-----VDDTIGVKVDYAGSFGDAKAGKTIAAQAAGAD--VIYQAAGGT 225
 QY 270 LTFEFSITIANQDR-----YLIQVDTDQ--SLVYT---KTKNKFSTILKNLGYSVF 317
 DB 226 GAGVFNEAKAINEKRSADKRWVIGVDRDQDEGKYSKDGKCANFVLASSIKEVGKAVQ 285
 QY 318 SVLSDLTYTKKSNRNLAGFEFGKKSATVYIGIKDRFVDIADTSLBGNDKLATEAISEAK 377
 DB 286 LINKQVADK-----FPGK--TTVY-GLKDGVEIATY---NVSKEAVKAIKEAK 330

RESULT 6 US-10-451-337-41

Sequence 41, Application US/10451337
 Publication No. US20040097706A1
 GENERAL INFORMATION:
 APPLICANT: SHIRE BIOCHEM INC.
 APPLICANT: MARTIN, Denis
 APPLICANT: BRODEUR, Bernard R.
 APPLICANT: HAMEL, Josee
 APPLICANT: RIOUX, Stephane
 APPLICANT: RHEAULT, Patrick
 TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS AND
 TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
 FILE REFERENCE: 12806-24PCT
 CURRENT APPLICATION NUMBER: US/10/451,337
 CURRENT FILING DATE: 2003-11-18
 PRIOR APPLICATION NUMBER: US 60/256,940
 NUMBER OF SEQ ID NOS: 42
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 41
 LENGTH: 330
 TYPE: PRN
 ORGANISM: S. pyogenes
 US-10-451-337-41

Query Match 10.0%; Score 216.5; DB 15; Length 330;
 Best Local Similarity 28.3%; Pred. No. 4.7e-08;
 Matches 102; Conservative 46; Mismatches 143; Indels 69; Gaps 17;

QY 39 AAKADANKHFGMLNAIYTAGTVNDNSFNOSGMEALIQOLGALTG-GEITSVDSSTAIEG 97
 DB 19 ASKGAAGKTDLKVAMVTDGVDKSPNOSAMEGLQSKGEMGLQKGTGDFYQSTSES 78
 QY 98 KYSLANTNNKVVVLSGFQ--HGDAFTRWLKIPEKNKILIGIDMTDTEVNIPT 155
 DB 79 EYA-----TNDTAVSGGYQLYIGIGA--LKDAIAKAGNDEGVKVIID----DIEGK 128
 QY 156 GRVINTLYKTEBAGMLAGVNASFLAKKPSDPTKRSAL-VIGGISPATVDTPIAGYIAG 214
 DB 129 DNVAATVPADHEAAYLAGIAAK-----TTKTTGVPVGMGEGTVITREKGEAG 179
 QY 215 IKAWNLKNSDKKITTDDKIEINLGF----DVODSTKERLEQIASKDKPSTLLAVAGP 269
 DB 180 VKS-----VDDTIGVKVDYAGSFGDAKAGKTIAAQAAGAD--VIYQAAGGT 225
 QY 270 LTFEFSITIANQDR-----YLIQVDTDQ--SLVYT---KTKNKFSTILKNLGYSVF 317
 DB 226 GAGVFNEAKAINEKRSADKRWVIGVDRDQDEGKYSKDGKCANFVLASSIKEVGKAVQ 285
 QY 318 SVLSDLTYTKKSNRNLAGFEFGKKSATVYIGIKDRFVDIADTSLBGNDKLATEAISEAK 377
 DB 286 LINKQVADK-----FPGK--TTVY-GLKDGVEIATY---NVSKEAVKAIKEAK 330

Db 82 ESEYA-----TNLPTAVSGYQLIYIGIFA--LKDAIAKAGDNGVKFVIIIDDIIEGKD-- 133
 Qy 148 DTEVIVPTGAYINULTYTEBAGWLAGYANASFLAKKPPSPPTKSAIVIGGISPATDF 207
 Db 134 ---NV-----ASVTFADHEAAVYLAGIAAK-----TTTKRTVGFVGGMEGYIYTR 175
 Qy 208 IAGYLAGIKAMNLKNSDKKTKITTDKIEINLGF-----DVODSTKRLLEQIASDKPRST 262
 Db 176 FEFGEAGVKS-----VDDTIQVAVDVAGSGDAAKGTIAAAYAAAGAD--VI 221
 Qy 263 LLAVALGELTEIFSDIIANON---DR-YLIGVDTDQ--SLVYT---KTKNKEFTSLKN 311
 Db 222 YQAAGGTGAGVFNAAINERKSEADKVMVIGVDRDQDEKGYTSKDGKEANFVLASSIKE 281
 Qy 312 LGYSVFEVSLDLYTKKNSRNLAGFEFGKKSATVYLGIDKRFVDIADTSLEGNDKXATE 371
 Db 282 VGRAVQIINKOVADR-----FPGGK--TIVY-GLKGGVGIATT---NVSKEAVK 325
 Qy 372 AISEAKKEFEKTKTIP 388
 Db 326 AIKAKAKIKSGDIKVP 342

RESULT 10

US-09-765-272-8
 ; Sequence 8, Application US/09765272
 ; Patent No. US20020061545A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Choi et. al.
 ; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccine
 ; NUMBER OF SEQUENCES: 452
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
 ; COMPUTER: HP Vectra 486/33
 ; OPERATING SYSTEM: MSDOS version 6.2
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/765,272
 ; FILING DATE: 22-Jan-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/961,083
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brookes, A. Anders
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: P3340P2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 328 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 ; US-09-765-272-8

Query March 9.4%; Score 202; DB 9; Length 328;
 Best Local Similarity 25.7%; Pred. No. 5.9e-07;
 Matches 98; Conservative 55; Mismatches 145; Indels 84; Gaps 19;
 Qy 33 RKSEIMAKADANHFGLNMAIVTAGTVNDSFNQSGWEAIIQOLGA---LTGSEITSVD 89

Db 3 RSSRNMASSSDVK-----TKAAIVTDGVDKSPFQSGAMEGLQAWGKEHNLSDKNGFTYP 58
 Qy 90 SSTAELE-----GKYSLLANTKNVWVLSGFQHGDAFTWLKIPENKOLFTEKNII 140
 Db 59 QSTSEADYANNLQQAAGSYNLIFGV-----GFALNNA-----VKDAKKEHTDLNIV 104
 Qy 141 ILGIDWTDENVIPTRGYINULTYTEBAGWLAGYANASFLAKKPPSPPTKSAIVIGGI 200
 Db 105 LIDVIRKQGNV-----ASVTFADNESGYLAGVAAK-----TTTKQVGFVGGI 149
 Qy 201 -SPAVTDFIAGYLAGIKAMNLKNSDKKTKITTDKIEINLGFVDVODSTKRLLEQIASDK 259
 Db 150 ESEVISRFEAGFRAGV-----ASVDSPIKQVAVAG-SFG-DAKAGKTIAAAYAAAGAD- 201
 Qy 260 PSTLLAVAGPL-TEIFSDIIANONDR-----YLIGVDTQSL--VYT-----KTKNKEFT 306
 Db 202 -IIVQVAGGTGAGVFNAAINERKSEADKVMVIGVDRDQDEKGYTSKDGKESNVLV 259
 Qy 307 SILKNLGYSVFSVSLDLYTKKNSRNLAGFEFGKKSATVYLGIDKRFVDIADTSLEGNDK 366
 Db 260 STLKQVGTIVKDI-----SNKAERGEFPGGQ---VIYYSJKDGVDLAVTNLSSEBK 308
 Qy 367 KLATEAISEAKKEFEKTKTIP 388
 Db 309 K---AVEDAKAKILDSGVKVP 326

RESULT 11

US-09-769-787-132
 ; Sequence 132, Application US/09769787
 ; Publication No. US20030091577A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Microbial Technics Limited
 ; APPLICANT: Gilbert, Christophe FG
 ; APPLICANT: Hansbro, Philip M
 ; TITLE OF INVENTION: Proteins
 ; FILE REFERENCE: PWC/22129WC
 ; CURRENT APPLICATION NUMBER: US/09/769,787
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: GB 9816337.1
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: US 60/125164
 ; PRIOR FILING DATE: 1999-03-19
 ; NUMBER OF SEQ ID NOS: 388
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 132
 ; LENGTH: 350
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 ; US-09-769-787-132

Query March 9.4%; Score 202; DB 10; Length 350;
 Best Local Similarity 25.7%; Pred. No. 6.4e-07;
 Matches 98; Conservative 55; Mismatches 145; Indels 84; Gaps 19;
 Qy 33 RKSEIMAKADANHFGLNMAIVTAGTVNDSFNQSGWEAIIQOLGA---LTGSEITSVD 89
 Db 25 RSSRNMASSSDVK-----TKAAIVTDGVDKSPFQSGAMEGLQAWGKEHNLSDKNGFTYP 80
 Qy 90 SSTAELE-----GKYSLLANTKNVWVLSGFQHGDAFTWLKIPENKOLFTEKNII 140
 Db 81 QSTSEADYANNLQQAAGSYNLIFGV-----GFALNNA-----VKDAKKEHTDLNIV 126
 Qy 141 ILGIDWTDENVIPTRGYINULTYTEBAGWLAGYANASFLAKKPPSPPTKSAIVIGGI 200
 Db 127 LIDVIRKQGNV-----ASVTFADNESGYLAGVAAK-----TTTKQVGFVGGI 171
 Qy 201 -SPAVTDFIAGYLAGIKAMNLKNSDKKTKITTDKIEINLGFVDVODSTKRLLEQIASDK 259
 Db 172 ESEVISRFEAGFRAGV-----ASVDSPIKQVAVAG-SFG-DAKAGKTIAAAYAAAGAD- 223
 Qy 260 PSTLLAVAGPL-TEIFSDIIANONDR-----YLIGVDTQSL--VYT-----KTKNKEFT 306

Db 224 --IYYVAGGTGAGVFAEAKSLNESRPNENKRWVIGVDRDOEABGKTYTSKDKESNFTLV 281
QY 307 SILKNLGYSPVSLDLYTKKSNRNLAGFEFGKKSATVYIGIDRFVDIADTLEGNK 366
Db 282 STLQVGTTVVDI-----SNKAERGFPGQ---VIYVSLDKGVDLVTLNISEBK 330
QY 367 KLAETAISEAKKEFEKTKTIP 388
Db 331 K---AVEDAKAKILDSGVKVP 348

RESULT 12
US-09-071-035-80
; Sequence 80, Application US/09071035
; Publication No. US20020045737A1
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis polynucleotides and polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071.035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-071-035-80

Query Match 8.3%, Score 178; DB 9; Length 339;
Best Local Similarity 25.1%; Pred. No. 4e-05;
Matches 103; Conservative 51; Mismatches 140; Indels 116; Gaps 20;

QY 33 KSEIIMAKADANKHFGILNMAIVTAGTVNDNSFNQSGWEAIIQOLGA---LTGE----- 84
Db 7 KTAESGGGKDA---AHSAVIITDTGVDKSFNQSWEGLQWKGKHDLPESKGYAY 62
QY 85 ITSVDSS--TALEGGKSSLANTNKNVWVLSGFQHGDAFTRWLKIPEKNQLFTEKNIIIL 142
Db 63 IQSDADADYTTNIDQAVSKFNITFGI---GYLIKDA-----ISSAADANPDITNFI 112
QY 143 GIDMTDENVIPTGRYINLTYKTEBAGWLAGYANASFLAKKFPSPDPTKRSATVIGGIGSP 202
Db 113 DDQIDGKKNV-----VSATFRDNDAAYLAGVAAA-----NETKTNKVGFGGEG 157
QY 203 AVTP-FLINGLAGIKAMNLKNSDKKTKTTDKIRIINLGFVDQDTSTKERLEQIAKSKDPS 261

Db 158 VVIDFOAGFEKGV-ADAAVELGKEITVFI-----KTAASFADPA 196
QY 262 TLAVAGPLTEIFSDII-----ANQNR-YLIGVDTDQSL--VYT 298
Db 197 KGRALAAAMQNGVDIIIFHSGATGGVFPQEAQKLNSSGDKVWVIGVDRDOADQKX- 255
QY 299 KTK-----NKFPISILKNLGYSPVSLDLYTKKSNRNLAGFEFGKKSATVYIGIDRF 353
Db 256 KTKDGEKDNFTLITSLKGVGTAVQDIANRALDEK-----FPGSEHLVY-GLDKGG 304
QY 354 VDIADTSLBGNDDKLAETAISEAKKEFEKTKTIPAEVVKLTLEIPMPD 403
Db 305 VDLTDGYL--NDKT-----KEAVKAKDKVIGSDVAVPEKPE 339

RESULT 13
US-10-206-576-80
; Sequence 80, Application US/10206576
; Publication No. US20030017495A1
; GENERAL INFORMATION:
; APPLICANT: Choi et al.
; TITLE OF INVENTION: Enterococcus faecalis polynucleotides and polypeptides
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: Dell Latitude
; OPERATING SYSTEM: Windows 98
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/206.576
; FILING DATE: 29-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/071.035
; FILING DATE: 1998-05-04
; APPLICATION NUMBER: US 60/046.655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: US 60/044.031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: US 60/066.009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Hyman, Mark J.
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB369P1D1
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-206-576-80

Query Match 8.3%, Score 178; DB 14; Length 339;
Best Local Similarity 25.1%; Pred. No. 4e-05;
Matches 103; Conservative 51; Mismatches 140; Indels 116; Gaps 20;

QY 33 KSEIIMAKADANKHFGILNMAIVTAGTVNDNSFNQSGWEAIIQOLGA---LTGE----- 84
Db 7 KTAESGGGKDA---AHSAVIITDTGVDKSFNQSWEGLQWKGKHDLPESKGYAY 62
QY 85 ITSVDSS--TALEGGKSSLANTNKNVWVLSGFQHGDAFTRWLKIPEKNQLFTEKNIIIL 142
Db 63 IQSDADADYTTNIDQAVSKFNITFGI---GYLIKDA-----ISSAADANPDITNFI 112

QY 143 GIDWTDENVIPGRYINLTYTEAGMLAGYANASFLAKKFPSPDKRSATVIGGISP 202
 DB 113 DDQIDGKKNV-----VSATFRDNEAAYLAGVAAA-----NETKTKVGVGGE 157
 QY 203 AVTD-PIAGYLAGIKAWNKNKSDKKTITTDKIEINLGFVDQSTKERLEQIASKDKPS 261
 DB 158 VVIDRFQAGFEKGV-ADAAKEIGKEITVDI-----KYAASPADPA 196
 QY 262 TLAVAGPLTEIFSDII-----ANQNR-YLIGVDTQSL--VYT 298
 DB 197 KGRALAAAYQNGVDIIFHSGATGCGVFEAKDLNMSGGDKVWIGVDRDQADGKY- 255
 QY 299 KTK-----NKFFTSILKNLGYSPVSLDYTKKSNRNLAGFEFGKKSATVYLGIDRF 353
 DB 256 KTDGKEDNFTLTSLTGAVGTAVODIANRLAEDK-----FPGEHLVY-GLMDGG 304
 QY 354 VDIADTSLBGNDKKLATBAISEAKKEFEKTKTIPAEVRKLTLEIPMPD 403
 DB 305 VDLTDGYL--NDKT-----KEAVKTAKDVKVIGDVKVPKPE 339

RESULT 14

US-09-071-035-78
 ; Sequence 78, Application US/09071035
 ; Publication No. US20020045737A1
 ; GENERAL INFORMATION:
 ; APPLICANT: G11 H. Choi
 ; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
 ; NUMBER OF SEQUENCES: 496
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
 ; COMPUTER: HP Vectra 486/33
 ; OPERATING SYSTEM: MSDOS version 6.2
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/071,035
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: A. Anders Brookes
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PB369P2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 78:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 361 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-071-035-78

Query Match

Best Local Similarity 8.3%; Score 178; DB 9; Length 361;
 Matches 103; Conservativity 51; Mismatches 140; Indels 116; Gaps 20;

QY 33 KSEIIMAAKADANGHFLNMAIYTAGTVNDNFGSGWEIIOQLGA---LTGE----- 84
 DB 29 KTAESGGGKDA---AHSAVIITDTGTGVDKSPNOSWGLQAMGKHDLPEGSKGVAY 84

QY 85 ITSVDSS--TAELEGXSSLANNTNKNVWVLSGFQHGDAFTRMUKIPENKOLFTEKNIIIL 142
 DB 85 IQSNDADYTTNIDQAVSSKFTITFGI-----GYLKKDA-----ISSAADANPPTNVL 134
 QY 143 GIDWTDENVIPGRYINLTYTEAGMLAGYANASFLAKKFPSPDKRSATVIGGISP 202
 DB 135 DDQIDGKKNV-----VSATFRDNEAAYLAGVAAA-----NETKTKVGVGGE 179
 QY 203 AVTD-PIAGYLAGIKAWNKNKSDKKTITTDKIEINLGFVDQSTKERLEQIASKDKPS 261
 DB 180 VVIDRFQAGFEKGV-ADAAKEIGKEITVDI-----KYAASPADPA 218
 QY 262 TLAVAGPLTEIFSDII-----ANQNR-YLIGVDTQSL--VYT 298
 DB 219 KGRALAAAYQNGVDIIFHSGATGCGVFEAKDLNMSGGDKVWIGVDRDQADGKY- 277
 QY 299 KTK-----NKFFTSILKNLGYSPVSLDYTKKSNRNLAGFEFGKKSATVYLGIDRF 353
 DB 278 KTDGKEDNFTLTSLTGAVGTAVODIANRLAEDK-----FPGEHLVY-GLMDGG 326
 QY 354 VDIADTSLBGNDKKLATBAISEAKKEFEKTKTIPAEVRKLTLEIPMPD 403
 DB 327 VDLTDGYL--NDKT-----KEAVKTAKDVKVIGDVKVPKPE 361

RESULT 15

US-10-206-576-78
 ; Sequence 78, Application US/10206576
 ; Publication No. US20030017495A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Choi et al.
 ; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
 ; NUMBER OF SEQUENCES: 497
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: CD-R
 ; COMPUTER: Dell Latitude
 ; OPERATING SYSTEM: Windows 98
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/206,576
 ; FILING DATE: 29-Jul-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/071,035
 ; FILING DATE: 1998-05-04
 ; APPLICATION NUMBER: US 60/046,655
 ; FILING DATE: 1997-05-16
 ; APPLICATION NUMBER: US 60/044,031
 ; FILING DATE: 1997-05-06
 ; APPLICATION NUMBER: US 60/066,009
 ; FILING DATE: 1997-11-14
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hyman, Mark J.
 ; REGISTRATION NUMBER: 46,789
 ; REFERENCE/DOCKET NUMBER: PB369P1D1
 ; INFORMATION FOR SEQ ID NO: 78:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 361 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-10-206-576-78

Query Match

8.3%; Score 178; DB 14; Length 361;

Best Local Similarity 25.1%, Pred. No. 4.4e-05;
Matches 103; Conservative 51; Mismatches 140; Indels 116; Gaps 20;

```

Qy      33 RKSEIMAKADANHFGLNMAIVTAGTVNDNSFNQSGWEAIOQLGA---LTGGE----- 84
      29 KTAESGGKGDH-----AASAVIITDTGVDKSFNQSWEGLQAMGKEHDLPEGSKGYAY 84
Db
Qy      85 ITSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKI PENKQLFTEKNIIIL 142
      85 IQSNDADYFTTNIDQAVSSKEFTIIFGI---GYLLKDA-----ISSNADANPDNFEVLI 134
Qy      143 GIDWTDTEENVIFPTGRYINLTYTEEAGWLAGYANASFLAKKFPSPDPTKSAIVIGGGISP 202
      135 DDQIDGKKNV-----VSATFRDNEAAYLAGVAAA-----NETKTNKRVGVGGE 179
Db
Qy      203 AVTD-FLAGYLGIKAWMLKNSDKTKITTDKIRINILGFDVQDTSTKERLEQIASDKDPS 261
      180 VVIDRFQAGPEKGV-ADAKELGKEITVDT-----KYAASFADPA 218
Db
Qy      262 TLLAVAGPLEIFSDII-----ANQNDR-YLIGVDTQSL--VYT 298
      219 KQKALAAAMYONGVDIIFHASGATGGVFCQAKDLNESGSGDKYVIGVDRDQDADGKY- 277
Db
Qy      299 KTK-----NKEFTSILKNLGYSVFSVLSDLTYTKKNSRNLAGFBEKKSATVYLGIDRF 353
      278 KTKDGKEDNFTLTSTLKGVGTAQODIANRALEDK-----FPGGEHLVY-GLKDDG 326
Db
Qy      354 VDIADTSLGNDKKLATEAISAEAKKEFEKTKTI PAEEVRKTLTEIPEMPD 403
      327 VDLTDGYL--NDKT-----KEAVKTAQDKVISGDAVPEKPE 361
Db

```

Search completed: December 18, 2004, 01:44:03
Job time : 98.7643 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 18, 2004, 01:15:13 ; Search time 25.651 Seconds
(without alignments)
1586.669 Million cell updates/sec

Title: US-09-676-249D-4

Perfect score: 2155
Sequence: 1 MWDKERTKEKESADNQNKOI.....KOPDKQOESLDKLTIDNNL 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match	Length	DB ID	Description
1	552	25.6	461	2 B90555	ABC transporter xy
2	203.5	9.4	350	2 F86804	basic membrane pro
3	202	9.4	350	2 G95097	lipoprotein (impor
4	198	9.2	374	2 C97965	conserved hypochet
5	192	8.9	357	2 D96986	probable lipoprote
6	181	8.4	353	1 H71340	membrane lipoprote
7	180.5	8.4	350	1 C70009	ABC transporter (1
8	178.5	8.3	359	2 F72418	basic membrane pro
9	177	8.2	341	2 E70147	basic membrane lip
10	173	8.0	357	2 AH1610	CD4+ T cell-stimul
11	168.5	7.8	357	2 C82946	hypothetical prote
12	168	7.8	357	2 AD1248	CD4+ T cell-stimul
13	165.5	7.7	360	2 H70147	basic membrane pro
14	162.5	7.5	525	2 C82914	conserved hypochet
15	161	7.5	339	2 F70147	basic membrane pro
16	152.5	7.1	591	2 D64204	hypothetical membr
17	150	7.0	524	2 D82944	membrane lipoprote
18	146	6.8	353	2 G70147	basic membrane pro
19	140	6.5	379	2 H75318	membrane lipoprote
20	139.5	6.5	337	2 AH2591	membrane lipoprote
21	139.5	6.5	337	2 B97374	Deinococcus radiot
22	136	6.3	547	2 E29504	mercury (II) reduct
23	134	6.2	539	2 D82886	conserved hypochet
24	132	6.1	326	2 G95857	hypothetical prote
25	131.5	6.1	1558	2 B71603	RSA-H3 antigen PF
26	128	5.9	657	2 S73428	probable lipoprote
27	126	5.8	349	2 F84246	hypothetical prote
28	125.5	5.8	763	2 A82863	hypothetical prote
29	125.5	5.8	1223	2 E88451	protein K10D2.1 (1

30	123.5	5.7	626	2 C25035	Colicin Ia - Bache
31	122.5	5.7	322	2 F84236	ABC transporter (1
32	122.5	5.7	2346	2 T13829	Tpr homolog - Eru1
33	120	5.6	1546	2 G90603	hypoprotein (impor
34	119.5	5.5	384	2 I40867	hypothetical prote
35	119.5	5.5	2285	2 T12796	probable transglyc
36	118.5	5.5	556	2 H82301	peptide ABC transp
37	118.5	5.5	1140	2 S73786	hypothetical prote
38	118.5	5.5	1963	2 B98002	Iga-specific metal
39	118	5.5	1031	2 C81302	probable type I st
40	117	5.4	798	2 S62791	probable lipoprote
41	117	5.4	1959	2 AG1085	hypothetical prote
42	116.5	5.4	396	2 AD2719	conserved hypochet
43	116.5	5.4	396	2 H97500	hypothetical prote
44	115.5	5.4	350	2 F70139	exported protein (
45	115	5.3	282	2 C97271	probable xylanase/

ALIGNMENTS

RESULT 1

B90555 ABC transporter xylose-binding lipoprotein [imported] - Mycoplasma pulmonis (strain UAB (

C/Species: Mycoplasma pulmonis

C/Date: 24-May-2001 #sequence_revision 24-May-2001 #ext_change 09-Jul-2004

C/Accession: B90555

R/Champan, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A/Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmk

A/Reference number: A99512; PMID:11353084

A/Accession: B90555

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-461 <KUR>

A/Cross-references: UNIPROT:Q980U5; GB:AL445566; P1D:G14089760; P1DN:CAC13519.1; GSPDB:GT

A/Experimental source: Strain UAB C11P

A/Genetic:

A/Gene: MYPU 3460

A/Genetic code: SGC3

Query Match 25.6%; Score 552; DB 2; Length 461;
Best Local Similarity 31.2%; Pred. No. 1.5e-26;
Matches 133; Conservative 82; Mismatches 161; Indels 50; Gaps 11;

QY	13	ADNQNKOIT--DYSKISGLVNER-----KSEITMAKADANKHGLNMAITVAGTV 61
DB	28	AONPNKINSMLDSSKTIIDLSQKEVETQKIYENKIKQASLEFQK-----VLTITADGNI 82
QY	62	NDNSFNQSGWEALQOLGALTGEITS-----VDSSTALEGKYSSLANTNK 107
DB	83	DDISFNQVYESQKTLKDPDYKAYKSONKEAENQHKLDNYINAVKDLQENVKVALDRGY 142
QY	108	NWVSLSGFGQGDFTMLKLPENKQLFTEKNIIILIGDWTDTEN-VIPTGRYINLTYTE 166
DB	143	TTVILITGFOQGNIEFLENDENNLRPEKKNKVIIGVMAPNNSKIPQSSLSLEKTE 202
QY	167	EAGMLAGYANASFLAKKPSDPTKRSALIVGGISPAVTFPIAGYLAGIRAMN--LKNSD 224
DB	203	EAGMAGYASADLVGTYKIANNEAKRAISAFGGDFACVTFPLNGFEGDIANNSSEANAN 262
QY	225	KKTITTDKIEINLGPVDVDTSTKERLEQIASKQKPESTLLAVAGPLTEIFSII--ANQ 281
DB	263	KKTKIVSENLVLTGF-IPNAEKNEVSVNVERGKSTISLPVAGPFGVAVDLRKQTSO 321
QY	282	NDRLIIVDTPDQSLVYTKTKNKEFTSLKVLGYSVSVLSDIYT-----KKSNSRNL 333
DB	322	EDFFIVGVDPDQSLVYTKTKNKEFTSLKVLGYSVSVLSDIYT-----KKSNSRNL 381
QY	334	AGFEFGKSAIVYLGIDRFVADTSLSEGNKKLATEAISEA--KKEFEKTKTIPAE 391
DB	382	GS--NPKNLVLRKGLSAKFAVNITKSKVKSITQADTSIQKALDKMANPNNSKILEKM 438

QY	392 VRKTL	397
Db	439 TNGDL	444

RESULT 2

basic membrane protein A [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
 C:Species: *Lactococcus lactis* subsp. *lactis*
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C:Accession: F86804
 R:Botolin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: F86804
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-350 <STD>
 A:Cross-references: UNIPROT:O9CFM9; GB:AB005176; PID:gl2724428; PIDN:AAK05536.1; GSPDB:C
 A:Experimental source: strain IL1403
 C:Genetics:
 C:Gene: bmpA

Query Match	9.4%;	Score 203.5;	DB 2;	length 350;
Best Local Similarity	24.7%;	Pred. No. 2.7e-05;		
Matches 97;	Conservative 63;	Mismatches 157;	Indels 75;	Gaps 17;

```

QY      2  IYDSKISGLVNRKEBIMAAKADANKHGLMMAIVTAGVYVNNSPFQSGWELIQQDGA  79
Db      13  LASVAIVLAGGRSHDAAGSGRAKTD-----LAAALVTEIGGVNDRSPFQSGWELIQQSGWK  66
QY      80  LTG-----GEITSVDSSTAELBGRKYSLSLANTKNWVLSGCFQHGGAFTRWMLKIPENQOLF  134
Db      67  ENNLKKGTGYTYYQNSASADYTTNNNSMAQQGYKLLPFGTSGLSDDAHSAAK---NN---  120
QY      135  TEKNIIILGIDWTDTENVIPTRGYINLTYKTEBAGMLAGVANASFLAKKPPSPPTKRSAI  194
Db      121  PKSNFVYIVDSVIMKDOQNV-----ASATPADNESAYLAGVAALK-----ATKTNKI  165
QY      195  -VIGGGISPAVNDIFINGLYLAGIKANMLKNKSDKTKITTDKIBINLGFVDQPTSKHELEQ  253
Db      166  GFIIGGQOSDVITTRFEKGYEAGAKSVN-----PDIKVDVYAGSFSDDAAKGITIAA  215
QY      254  IASKDRPSTLLAVAGPL-TEIFSDIIA-----NQNDR-YLIGVDPDQSLV--YT-----KT  300
Db      216  AMTGAAGDDVYQCAAGVGCTGVSEAKALNSTGNEADKRWVIGVDDODEYLGKTYSKSGKD  275
QY      301  KKKFFTSILKNLGVSVFSVLSDLVYTKKSNRNLAC--FEFGKSAAYYLLGIKORFYVDIAD  358
Db      276  SNFVLVSTIKEVG-----NVVKDIADIKTKDGRKPGGTIVTYDLKKGGVNLGL-----DSAN  326
QY      359  TSLGNDKLLATALISAKKEFEFEKTKTTPAE  390
Db      327  SEIK-----DAVAKAKADIIDGKITVPSK  350

```

RESULT 3

1|lipoprotein [imported] - Streptococcus pneumoniae (strain TIGR4)
C|Species: Streptococcus pneumoniae
C|Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
A|Accession: G95097
R|Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
son, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickney, E.R.; Holt, I.E.
Science 293, 498-506, 2001
A|Authors: Iottus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A|Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.
A|Reference number: A95000; MUID:21357209; PMID:11463916
A|Accession: G95097
A|Status: preliminary
A|Molecule type: DNA

A:Residues: 1-350 <KUR>
A:Cross-references: UNIPROT:Q97RH0; GB:AE005672; PDB:1AAK74976.1; PID:g14972319; GSPDB:G1
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0845
C:Superfamily: ABC transporter ynfN

Query Match	9.4%	Score 202;	DB 2;	Length 350;
Best Local Similarity	25.7%;	Pred. No. 3.3e-05;		
Matches 98;	Conservative 55;	Mismatches 145;	Indels 84;	Gaps 19;

```

QY 33 RSEIIMAAADANKHGLMMAIVTAGIVDNSEFNOSGFEAIIOQLA---LITGEIITSVD 89
Db 25 RSRNRNAASSDVK---TKAAIVTDTGTGVDDKSFFNOSAMGLOAMGXEHNLSKONGFYTF 80
QY 90 SSTAEL-----GKYSILANTNKNVWVLSGFQHDATFTRMLKIPENKQLEFTEKNII 140
Db 81 QSTSEADYANNLQQAAGSYNLI.FGV-----GFLNMNA-----YKDAKEHTDLNIV 126
QY 141 ILGIDMTDTENVIPTGRYINLTYKTEEAGMLAGYANASPLAKKFPSPPTKRSALVIGGI 200
Db 127 LIDVDIAKQQKNV-----ASVTFPADNESGYLAGVAAAK-----TTTKQGVFWGGI 171
QY 201 -SPATYDFLAGLAGIKAMNKLKSDDKKITTDKIEINLGFVDYDSTTKERLEQIASDX 259
Db 172 ESEVSRFEPAGKAGV---ASVDPSIKQVDPYAG-SFG-DAKAGKTAAAOQAAGAD- 223
QY 260 PFTLLAVAGPL-TEIFSDIILANONDR-----YLIGVDTOQSL--VYT---KTKNKPEFT 306
Db 224 --IVYQVAGGTGAGVAAEAKSLNESRPENEKAVWIVGDRQDEAGKTTSDGKESNFWLV 281
QY 307 SILKNLGYSVFSVLSDDLTYTKKSNSRNLAGFEFGKKSATVYLGIKDRFPVADIADTSLEGNDK 366
Db 282 STLKQGVTTVKDI-----SNKARGEPPGQ---VIVYSLDKGVDLAVTNLSEBGK 330
QY 367 KLATEAISAEAKKEPEEKTITP 388
Db 331 K---AVEDAKAKIILDGVKVP 348

```

RESULT 4

conserved hypotoxinical protein spr0747 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: C97965
R:Host(s): J.A.; Albarn Jr., W.; Arnold, J.; Blaszczyk, L.; Buxgett, S.; Dehoff, B.S.; Edwards, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Meyer, P.; Sun, P.M.; Winkler, M.E.
Y: R: Bacteriol. 183, 5709-5717, 2001
A:Author(s): Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: C97965
A:Status: preliminary
A:Molecule type: DNA
A:Restructures: 1-3/4 <KUR>
A:Cross-references: UNIPROT:Q8DQC2; GB:AE007317; PID:AAK99551.1; PID:G15458340; GSPDB:GI
C:Genetics:
A:Gene(s): spr0747

Query Match	9.2%;	Score 198;	DB 2;	Length 374;
Best Local Similarity	25.4%;	Pred. No. 6.4e-05;		
Matches 97;	Conservative 54;	Mismatches 147;	Indels 84;	Gaps 18;

```

QY      33  RKSEIMAKAANHKHFLGMLNIVTAGGVYVNDSPFQSGMEALQOLGA---LTGGETITSV  89
Db      49  RSRRAAASSDVK---TKAAIVDTGTGVDKSPFQSGMEGLQAMGKHEINLSKDNQFYTF  104

QY      90  SSTALE-----GKYSLANTNKNVWVLSGFQHGDAFTRWLKIPIENKOLFTEKNII  140
Db      105 QSTSEADYANNIQQAAGSYNLI-----FGVGFALHNAVEEVAAEHNDLNV  150

```

141 ILGIDWTDTEENVIPTRGYINLTYKTEBAGLAGYANASFLAKKPPSPDKSAIVICGGI 200
151 LIDVDVADKQKVV-----ASVTFADNBSGYLAGVAALK-----TTKTKQVGFVGGI 195
201 -SPAVNDFIAGYLAGIYKAMNLSKSDKTKITTDKIEINLGFVODVDTSTKRLBQIAKDK 259
196 ESEVSIHSFEAGFKAGV-----ASVDPSTIKQVVDVAG-SFG-DAAKGKTIAAQVMAAD- 247
260 PSTLLAAGPL-TEIFSDIITANQNDR-----YLIGVDTQSL--VYT---KTKNKFET 306
248 --IVYQVAGGTGACVFAEASLSNBSRENKRVWIGVDRDDEAGKTKSDGKESNVLV 305
307 SILKNGVSVFVSLDLYTKKNSRNLAGFEFGKSAIVYLGIDRFVADIADTSLGNDK 366
306 STLKQVGTVMKI-----SNKAEKGFPGG---VIYVSLDKQGVDLAVTLVSEEGK 354
367 KLAIEASEAKKEFEKTKITP 388
355 K---AVEDAKAKILDSGVKVP 372

RESULT 5

D96986
probable lipoprotein, Med/BMP family [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: D96986
R;Nolling, J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: D96986
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-357 <KUR>
A/Cross-references: UNIPROT:Q97L60; GB:AE001437; PIDN:AAK78679.1; PID:G15023581; GSPDB:C
C/Experimental source: Clostridium acetobutylicum ATCC924
C/Genetics:
A/Gene: CAC0702

Query Match 8.9%; Score 192; DB 2; Length 357;
Best Local Similarity 23.3%; Pred. No. 0.00014;
Matches 94; Conservative 67; Mismatches 157; Indels 86; Gaps 18;
20 ITDVSISGLVNEKSEIIMAA--KADANKHGLMALVTAGCTVNDSPNOSGEALQOL 77
10 LTTVMIVAGLPAGCSSTSSGSGNSKDTKK--VKVGLSTDEGGLNDSFNGADEGIIKA 66
78 GALTGEITVDSSTA-ELBGKYSLLANTNKNVNLGSGFHGDAF-TRMLKIPENKOLFT 135
67 AKESYVDVYKAIKESKDDYQPNLOSLLDNDSLVFGVGYQMAADLAIKAKYPPKKAII 126
136 E-----KNIILIGIDWTDTEENVIPTRGYINLTYKTEBAGWLAGYANASFLAKKPSDP 188
127 DDADVQPKKII-----MSLVFKEQEGSFLMG-----VIAKGM----- 158
189 TKRSAL-VIGGISPATVDFIAGYLAGIKAMNLSKSDKTKITTDKIEINLGFVODVDTST 247
159 TKTNKIGFVGKQKPLNKPLSGYIAGAKTVN-----PNITVEK---NTNVSPTS 208
248 -KERLEQIASKDKSTLLAVAGPLTEIFSDIITANQNDR-----YLIGVDTQSLVYTTKTN 302
209 GKEVAATSLVNGCCDIYVHAAGAGAGIVF-DVAKSLRQGDVMAIGVDKQQAALPKYAD 267
303 KFTTSLKNGVSVFVSLDLYTKKNSRNLAGFEFGKSAIVYLGIDRFVADIADTSL 362
268 VILTSWYKRVADIATYNTVLDLVKGGK-----FEGKGVES---FGKEDGVAVAPTS-- 315
363 GNDKLAIEASEAKK-----EFEKTKITIPAEVVR 393
316 --NKHVPEVSLVLDYKKAIIIDGKIVPDTVDAQFTKTDQIK 357

RESULT 6

H71340
membrane lipoprotein tmpr precursor - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 07-Aug-1998 #sequence_revision 07-Aug-1998 #text_change 09-Jul-2004
C/Accession: H71340; A43595; S29561
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetexback, T.; McDer
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A>Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; MUID:98332770; PMID:965876
A/Accession: H71340
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-353 <COL>
A/Cross-references: UNIPROT:P29724; GB:AE001211; GB:AE000520; NID:G3322582; PIDN:AA66530;
A/Experimental source: strain Nichols
R;Schouls, L.M.; van der Heide, H.G.J.; van Embden, J.D.A.
Infect. Immun. 59, 3536-3546, 1991
A>Title: Characterization of the 35-kilodalton Treponema pallidum subsp. pallidum recomb
A/Reference number: A43595; MUID:91372962; PMID:1894360
A/Accession: A43595
A/Molecule type: DNA
A/Residues: 1-10, 'A', 12-158, 'R', 160-353 <SCH>
A/Cross-references: GB:X57836; NID:948838; PIDN:CAA40968.1; PID:G581809
A/Note: this protein is shown to incorporate palmitic acid
C/Genetics:
A/Gene: tmpr; TP0319
A/Start codon: GTG
C/Superfamily: ABC transporter ynfN
C/Keywords: blocked amino end; lipoprotein; membrane protein; thiolester bond
P:1-20/Domain: signal sequence #status predicted <SIG>
P:21-353/Product: membrane lipoprotein tmpr #status predicted <MAT>
F:21/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted
F:21/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted

Query Match 8.4%; Score 181; DB 1; Length 353;
Best Local Similarity 23.7%; Pred. No. 0.00065;
Matches 86; Conservative 69; Mismatches 134; Indels 74; Gaps 17;

52 MAIVTAGTVNDSPNOSGEALQOLGALTGEITVDSST-ALBGKYSLLANTNKNV 110
42 VGMWTDSDGIDDKSFGNQVVEGSRFAQENNAKCKVTASTDAEYVPSLSAFADENMGIV 101
111 VLSGFQHGDAFTWMLKPEKQKLFTEKNIILIGIDWTDTEENVIPTRGYINLTYKTEAGW 170
102 VAGGSFLVEA-----VLETSARFPKQKFLVIDAVVQDRNV-----VSAVFGQNGSF 149
171 LAGYANASFLAKKPPSPDKSAI--VIGG--GISPAVDFIAGYLAGIKAMNLSKDK 226
150 LVGYA-AALAKK-----AKSAVGFIVGMEGMPL--FEGAFEGAVAAD----- 193
227 TKITTDKIEINLGFVODVDT-STKRLBQIAK--DKPSTLLAVAG---PLTEIFSDIT 278
194 -----PDIVVVEVANTSPDQKQALAAKLYDSGVNVIPOVAGGTGNGVIEARDR 246
279 ANQNDKRLIGVDTQSL--VYTTKAKKFTSILKNGVSVFVSLDLYTKKNSRNLAGF 336
247 LNDQVWVIGVDDQVMDGYDYSKSVLTSWYKRA-----DVAAEKISKAADGSPG- 300
337 EFGKSAIVYLGIDRFVADIADTSLGNDKLAIEASEAKKEFEKTKITIPAEVVKTL 396
301 -----GQSIMFGEDKAVGLPE-----ENPNLSAVMEKIRSEKTI-----VSKET 342
397 EIP 399
343 VVP 345

RESULT 7

C70009

R:Ojaimi, C.; Davidson, B.E.; Saint Girons, I.; Old, I.G.
 Microbiology 140, 2931-2940, 1994
 A:Title: Conservation of gene arrangement and an unusual organization of rRNA genes in
 A:Reference number: 140241; PMID:95111614; PMID:7812434
 A:Accession: I40242
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-44, 'A', 46-179 <RE2>
 A:Cross-references: GB:I35050; NID:9516591; PIDN:ACC41402.1; PID:9551744
 C:Superfamily: basic membrane protein C

Query Match 8.2%; Score 177; DB 2; Length 341;
 Best Local Similarity 26.7%; Pred. No. 0.0011;
 Matches 100; Conservative 59; Mismatches 124; Indels 92; Gaps 25;

QY 44 ANKPGFLMAIVAGGVNDNSFNQSGWEALIQGLTGEIITSVDSSTAELEGKYS-- 101
 DB 24 SSKKIKISMLV---DGLVDDKSFNSSANLRLKDPENIEVFS--CAISGVSSYV 78
 QY 102 --LANTNKN---VWVLSGFQHGDAFTRLKIPENKOLFTEKNII--ILGIDWTDENV 153
 DB 79 SDDLNLKRNSSDLILVGVMLTDA--SLVSESEPKI--SYGIDPIYDDVQIPENLI 133
 QY 154 PIGRYNLVYKTEBAGWLACY--ANASFLAKFPSPDFTKSAIVIG--GGISPAVTD-FI 208
 DB 134 A-----VPRVQGAFLAGYIAAKKSFSGK-----IGFQGMKGNIYDAFR 174
 QY 209 AGYLAGIKAMNLKNSDKKTIITDKIEINLGFVQDSTKERLEQIASK--DKPSTLLAV 266
 DB 175 YGESAKAKYAN-KDIEITISYNSPSFSDVIG-----RTLAKSYSGIDVIFH 221
 QY 267 AGPLTEI-FSDIIANQND-RYLIGVDTDSLVYTKTKNKFETSLIKLGYSVFSVLSDL 324
 DB 222 AALAGIIVETAKNLGDDYVIGADPOD--YLAPKN-FITSVIKIIGALVITGE-Y 277
 QY 325 TKKSNRNLAGFEFGKKSATVYLGKDRFVDIADTSLGNDKKLATEISAEKKEFEKT 384
 DB 278 IKNNVY-----WEGSK-----VWQGLRDGVIGLPMAN-----EF-EYI 310
 QY 385 KTIPIAEVKTLEIP 399
 DB 311 KYLERKIKNEIIVP 325

RESULT 10

CD4+ T cell-stimulating antigen, lipoprotein [imported] - *Listeria innocua* (strain Clp1)
 C:Species: *Listeria innocua*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AH1610
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fahl, H.; Jones, L.M.; Karch, U.
 Science 294, 849-852, 2001
 A:Authors: Krefel, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maloumnam, A.; Maok, C.; Schleuter, T.; Simoes, N.; Tixeret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A:Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AH1610
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <GLA>
 A:Cross-references: UNIPROT:Q92BW7; GB:AL592022; PIDN:CAC96656.1; PID:G16413898; GSPDB:C
 A:Experimental source: strain Clp11262
 C:Genetic: A;Gene: tcsA
 C:Superfamily: ABC transporter yuIN

Query Match 8.0%; Score 173; DB 2; Length 357;
 Best Local Similarity 24.2%; Pred. No. 0.0021;
 Matches 101; Conservative 61; Mismatches 138; Indels 118; Gaps 23;
 QY 27 SGLV-----NKRSEIMAAKANKHGLNMAIVTAGGVNDNSFNQSGWEALIQGL 78

DB 16 SGLVLAGCGSSSDDKS-----GDKKSKDFTVAVTTDGVDDBSFNQSAWEGLOKFG 69
 QY 79 ALV-----GGEITSVDSSTAELEGKYSLANTNKQWVLS-----GFGHGAFTRLK 126
 DB 70 KANDMEKTDGIVYLOSASBADYK-----TNLNTVRSYDYLIGYIKLAIIEVSK 123
 QY 127 -IPEKOLFTEKNIIILGIDWTDENVIPTRYNLVYKTEBAGWLAVYANASFLAKFP 185
 DB 124 QPKNQFAIVDDTI-----DDRNVVSG-----FKNDOSYLVGVVAG----- 163
 QY 186 SDPTKSAIVYGGGIPAVTD-FIAGYLAGIKAMNLKNSDKKTIITDKIEINLGFVQ- 243
 DB 164 --TTKTKVGFVGVGVAVIDREAGFTGVKA-----VNPQAQIDVQY 205
 QY 244 --DTSKERLEQIASDKS-----TLAVAGPLTEIFSDIIANQND-----YLIGVDT 291
 DB 206 ANDPAKADKQQAASSMSYGVUVITHAAGTNGVPAE-AKQLKKDPSRAVWVIGVR 284
 QY 292 DQ-----SLVYTKTKNKFETSLIKLGYSVFSVLSDLVYTKNSRNLAG-FEFGKKSAT 344
 DB 265 DQMDGKVYANDGKVNTLTSEIKRVDIAV-----DLAT-----RTKADDPFGGTFK 312
 QY 345 YVIGIDRFVDIADTSLGNDKKLATEISAEKKEFEKTIPIAEVKTLEIPEP 402
 DB 313 IEYGLDKDAVGLSE--HQNISKDVLAKE--EYKQIVDGD-----IKVPEKP 357

RESULT 11

C82946
 hypothetical protein U0012 [imported] - *Ureaplasma urealyticum*
 C:Species: *Ureaplasma urealyticum*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: C82946
 R:Glaser, J.I.; Leikowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 submitted to Genbank, February 2000
 A:Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a min
 A:Reference number: A82870
 A:Accession: C82946
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-516 <GLA>
 A:Cross-references: GB:AE002100; GB:AF222894; NID:G6898946; PIDN:AAF30417.1; GSPDB:GN001;
 A:Experimental source: serovar 3; biovar 1
 C:Genetic: A;Gene: U0012
 A:Genetic code: SGC3

Query Match 7.8%; Score 168.5; DB 2; Length 516;
 Best Local Similarity 25.1%; Pred. No. 0.0066;
 Matches 110; Conservative 65; Mismatches 167; Indels 97; Gaps 26;

QY 48 FGANMAIVNAGGVNDNSFNQSG--WEALIQGLALGEGITTSVDSSTAE-LEGKYSGLAN 104
 DB 17 FALGIIIVATSTCKTSLVYSGPYW-----TSPTSDDEGFTKYSMAS 62
 QY 105 TNNVWVLSGFQHGDAFTRLKIPENKQ--LFTK-----NIIIP-----GIDWTDENVIP 156
 DB 63 DGRBALMPGYQ-----PERLQNALVNDKDPNIIAILIDGVYNNNDKAEYK 112
 QY 157 --RYNLVYKTEBAGWLAVYANASFLAK--PSPDFTKSAIVIG--GISPA-VTDFI 208
 DB 113 ADVADVDFVVDAAFLGIIAAYVYMLNSQAVGAD--NKLTWGGYVGINAKTNTNYL 168
 QY 209 AGYLAGIKAMNLKNSDKTK--ITTDKIEIN-----GFPVQDSTKERLEQI 254
 DB 169 AGFDLGVKANETLKDKIKQEGTQETKWINVEQYVASESSAGGQSDSANAKKIIQEL 228
 QY 255 ASKQDSTLLAVAGPLTEI-FSDIIANQND-RYLIGVDTDSLVYTKTKNKFETSL 308
 DB 229 ITKG-ADLIIPVAVIPOVGIIVTAIATTSINVGIVGDAIENDQAI--NKTKDFINTH 285
 QY 309 L--KNLGYSVFSVLS--DLVYTKNSRNLAGFEFGKKSATVYIGI--KDRF--VDI 356


```

Qy 157 RYILUYKTEAGLAVAGVANSFLAKK---PSPPTKRSALVIGGJS---PATYDPIAG 210
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 124 RIASITIRADQAAFLAGIAAAYLANSNONVFGKD---NKLTWGSPGCHLPSTRIRIOG 179
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 211 YLAGIKAMNLSKNSDKTKITTDKIE---INL-----GFVDQDSTYKER--LEQIAS 256
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 180 FKFEIQANEMELKKNKYKQKOTENNEKEMINEQVAFATNYQSGDPSPISSDAKAIWNOIYS 239
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 257 KDRPSTLLAAGPLTEIFPSDIIANQNDR-YLIGVDTQSLVYTKNKKFP--TSILKNLG 313
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 240 -NNVDILPLVAPQIDYATTAASSKPIYVGVGDTEQELDDNTNKARISENNKSLANGK 298
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 314 YSVSVSUS--DLYTK-----KSNKNLNLAGEFEGKKSATVYLGIDRPFYDIADTS 360
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 299 TIISIVYRDLDFARKGALLKASBGAQOTNDINCKAAYKLGHTTASF--NKNQTYVD--NTA 354
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 361 L-----EGNDKKLATATISE-----AKKEFEKTKTIP 388
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 355 LVLSLSKAGHOYLDAIKLSGLKEVNDYKTVIIEIIQBDPLFKLLSQIGTKLDEVAITSQQ 414
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 389 AAEVRKTLLEIPEMF-----DKOPDKQCES 412
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 415 GDMWLKS-EYQDULPFIOQKMLGGLVYVDQKNELPYELSNSFLYLEKDPNNKQAS 468
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

RESULT 15

Nucleic acid sequence analysis of the gene encoding the outer membrane protein A (OmpA) of *Borrelia burgdorferi*. The gene was cloned from strain B31 and sequenced. The deduced amino acid sequence of the OmpA protein is compared with those of other Borrelia species. The results show that the OmpA protein of *B. burgdorferi* is highly conserved with those of other Borrelia species.

A:Accession: F70147; MUID:94327086; PMID:8050720
A:Title: Nucleotide sequence and analysis of the gene in *Borrelia burgdorferi* encoding the outer membrane protein A.
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-339 <RES>
A:Cross-references: GB:L24194; NID:g508420; PIDN:AA72406.1; PID:g508421
R:Olaimt, C.; Davidson, B.E.; Saint Girons, I.; Old, I.G.
Microbiology 140, 2931-2940, 1994
A:Title: Conservation of gene arrangement and an unusual organization of rRNA genes in the genus *Borrelia*.
A:Reference number: I40241; MUID:95111614; PMID:7812434
A:Accession: I40241
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 248-339 <RE2>
A:Cross-references: GB:LJ5050; NID:g516591; PIDN:AAC41401.1; PID:g516592
C:Genetics:
A:Gene: bnpA
C:Superfamily: basic membrane protein C

Query Match	7.5%	Score 161;	DB 2;	Length 339;
Best Local Similarity	22.8%;	Pred. No. 0.01;		
Matches	85;	Conservative	68;	Mismatches 136;
				Indels 84;
				Gaps 18
59	GTVNDNSFNQSGMEAIQQQLGALTGTGEITSVDST----	ALEEGKYSILANTNKNWVVL	SG	114

```

Db      37  GTFDKSNESALNGVKYKKEEFKLELVUKESSNSYSLDLEG---LWDAGDGLTWLIG 92
Qy      115  FOHGD-AFTRWMLKIPENKOLFTEKNNIIILIGDWTENTENVIPGRYINLTYKTEBAGMLAG 173
Db      93  YRFSIVAKVALQNDMDKAI-----IDPIYSNDIP-ANLVGMFPFRAQEGAFLTG 142
Qy      174  YANNSFLAKKEPSPDPTKSAIVIGGISAFAVTD-FIAGYLAGI KAWNLKNSDKKTYITTD 232
Db      143  YIAAUL-----SKTGKIGFLGIBEIVADARFYGEAGAKVAN-----KDIKISTQ 188
Qy      233  KI---EINLGFHDVODSTKERLEQIASKDKCESTLLAVAGPLTEIPSDIIANO--NDRYL 286
Db      189  YIGSFADLEAGRSVATRWYSDEID-----IHHAAIGGIGAIIVAKELSGCHYI 238
Qy      287  IGVDTDSGLVYTKTKQKEFTSLIKLVGSVFSVLDLYTKGNSRNLAAPEFKKSATAY 346
Db      239  IGVDEDQAYL--APDNVYISTTKKVGRL-----NIFP--SNHLKTNFEEGK--LIN 285
Qy      347  LGIKRPFDIADTSLBGNDKKLATAISAKKEPEKTKTIPABEAVRYKLTLEIEMFDPKQ 406
Db      286  YGLKEGVGVFV---RNPKMISF-----ELEKEINDLSKTIINKEIIVF----- 325
Qy      407  DKQGESLDKLITD 419
Db      326  -SNKESYEKFLKE 337

```

Search completed: December 18, 2004, 01:27:31
Job time : 27.651 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2004, 01:14:44 ; Search time 119.543 Seconds
(without alignments)
2035.941 Million cell updates/sec

Title: US-09-676-249D-4
Perfect score: 2155
Sequence: 1 MMDKTTKEKKSADNONKQI.....KQPKQOESLDTITDINNLL 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	693.5	32.2	457	2	Q48902 mycoplasma
2	552	25.6	461	2	Q980U5 mycoplasma
3	465.5	21.6	491	2	Q6K104 mycoplasma
4	465.5	21.6	491	2	QAT27522 mycoplasma
5	414.5	19.2	468	2	Q6E5B5 mycoplasma
6	391	18.1	465	2	Q9X775 mycoplasma
7	384.5	17.8	428	2	Q52311 mycoplasma
8	382.5	17.7	428	2	Q9RGX5 mycoplasma
9	379.5	17.6	428	2	Q32417 mycoplasma
10	379	17.6	428	2	Q9RGX4 mycoplasma
11	379	17.6	428	2	Q9RGX6 mycoplasma
12	377.5	17.5	428	2	Q9RGX7 mycoplasma
13	374.5	17.4	428	2	Q9RGX3 mycoplasma
14	373.5	17.3	428	2	Q9R3N6 mycoplasma
15	229.5	10.6	352	2	Q6RCH2 thermomanaer
16	229	10.6	457	2	Q6F0B8 mesoplasma
17	228	10.6	349	2	Q9E9V1 clostridium
18	221.5	10.3	350	2	Q878B8 streptococc
19	220.5	10.2	350	2	Q8K7C9 streptococc
20	220.5	10.2	350	2	Q992H4 streptococc
21	217.5	10.1	350	2	Q8P0W2 streptococc
22	217	10.1	349	2	Q8DZJ8 streptococc
23	217	10.1	349	2	Q8E5V9 streptococc
24	215	10.0	349	2	Q8DUJ6 streptococc
25	207	9.6	359	2	Q898S3 clostridium
26	203.5	9.4	350	2	Q9CFM9 lactococcus
27	202	9.4	350	2	Q97RH0 streptococc
28	198	9.2	374	2	Q8DOC2 streptococc
29	196	9.1	466	2	Q7WU1L epistolaema
30	195.5	9.1	347	2	Q8E1F0 streptococc
31	195.5	9.1	347	2	Q8E6W8 streptococc

32	193.5	9.0	361	2	Q81A05 bacillus ce
33	192	8.9	357	2	Q97L60 clostridium
34	187	8.7	368	2	Q8FX05 bruceella su
35	185.5	8.6	550	2	Q6MUL7 mycoplasma
36	185.5	8.6	550	2	Q6E7664 mycoplasma
37	183	8.5	325	1	BMPA_BORGA 01357 borrelia ga
38	182	8.4	348	2	Q9AK41 streptomyc
39	181	8.4	333	1	TMPC_TREPA P29724 treponema p
40	180.5	8.4	350	1	YUPN_BACSU 005252 bacillus su
41	178.5	8.3	359	2	Q9XV77 thermotoga
42	178	8.3	341	1	BMPB_BORBU 045011 borrelia bu
43	178	8.3	361	2	Q83918 enterococcu
44	177	8.2	337	2	Q8KWS0 borrelia bu
45	177	8.2	347	2	Q79YMS streptococc

ALIGNMENTS

RESULT 1

ID	Q48902	PRELIMINARY;	PRT;	457 AA.
AC	Q48902;			
DT	01-NOV-1996 (TREMBL)	01, Created		
DT	01-NOV-1996 (TREMBL)	01, Last sequence update		
DE	01-MAR-2004 (TREMBL)	26, Last annotation update		
DE	Ag 243-5 protein precursor.			
OS	Mycoplasma arginini.			
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.			
OX	NCBI_TaxID=2094;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=6163149; PubMed=8551970;			
RA	Uehio S., Iwaki K., Tanai M., Ohta T., Fukuda S., Sugimura K.,			
RA	Kurimoto M.,			
RT	"Metabolic promoting activity of a novel molecule, Ag 243-5 derived			
RT	from Mycoplasma and the determination of the complete nucleotide			
RT	sequence."			
RL	Microbiol. Immunol. 39:393-400(1995).			
DR	EMBL: D1674; BAA04082.1; -			
DR	GO: GO:0008289; F: lipid binding; IEA.			
DR	InterPro: IPR003760; Bmp.			
DR	Pfam: PF02608; Mycoplasma_p48.			
DR	PRINTS: PR01733; LIPPROTEIN48.			
KM	Signal.			
FT	1 25 Potential.			
FT	CHAIN 26 457 Ag 243-5 protein.			
SQ	SEQUENCE 457 AA; 50789 MW; 9AEBAB1620CB22F CRC64;			

Query Match 32.2%; Score 693.5; DB 2; Length 457;
Best Local Similarity 39.0%; Pred. No. 4.3e-35;
Matches 168; Conservative 81; Mismatches 141; Indels 41; Gaps 14;

QY	5	ETTKERSADNONKQITDVSKISGLVNERKSEIMAAKADANKHGLMAIVTAGTVNDN	64
DB	28	ETDKEGKII-----RIFD-----NSFVKDROAEIEKA-----KNDFVTALLTAGTVODK	73
QY	65	SFNOSGWEAT----QQLGALTG--GEITSVDSSTAELEKYSISLANTKNNVWSGFGHD	119
DB	74	SFNOSIWEAVLEHVDQJEKTTNLDKRSQETNNOSELGKTKNPLNGKNWIIILGFGQO	133
QY	120	AFRWMLKIPEN-----KQLPTEKNIIILGIDW---TDENVIPTRGRIINTYKTEAGWL	171
DB	134	EFPEFLKQTSNGKYSIDLAEKKVIVAVDMDSKDKDLIRAGHTISLTKTEAGFI	193
QY	172	AGVANASFLAKKPSDEPKSAIVTGGISPAVDTFAGYLAGI KAVNLKNSDKTKITT	231
DB	194	AGVASSKFLAVKFPNDKAKRTIAPFGGAGAGVTDFTAGYLAGI KAVNNNDPTAKVTISD	253
QY	232	DKIEINIGFDVQDTSTKEREQLASKDKBSTLAVAGPLTEIRSDII--ANQNDRYLIGV	289
DB	254	NNINIDTGF-ISNDKATFTINGIVNKS--SLVLPVAGSLTSSVVDALKSNKDKTKYLIIGV	310

```
QY 290 DTDOSLYVTTKNKKFFTSILKNLGYSVFSVLSDLTYTKSKNSRLNAGEFPGK---KSAIV 345
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 311 DTDOSKIFSPA-TVFETSIKHLRTIYQVLTDIWLKEDSKFLGSPRSFLTNPAIVATV 369
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 346 YLGIKDFVDIADTSLSEGNKKLATEAISAKKFEFEKTKITPABEVKRTKLEIPEM---P 402
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 370 YKGISDFFGVSNSTVADADKVKAKQEFLENTADFKQIQANPT-NYKSVGIPTMLIND 428
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 403 DKQDPKQOESL 413
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 429 NDADKNEKASL 439
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 2
Q980L5 PRELIMINARY; PRT; 461 AA.
ID 0980L5
AC 0980L5;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ABC TRANSPORTER XYLOSE-BINDING LIPOPROTEIN.
GN OrderedLocustNames=MYPV_3460;
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP;
RX MEDLINE=2167165; PubMed=11353084;
RA Chambud I., Dvbyig K., Wroblewski H., Vlati A., Rocha E.P.C.,
  Moszer I., Blanchard A.;
  "The complete genome sequence of the murine respiratory pathogen
  RT Mycoplasma pulmonis.";
  Nucleic Acids Res. 29:2145-2153(2001).
RL EMBL: A145564; CAC13519.1; -.
DR EMBL; B90555; B90555.
DR MyPulst; MYPV_3460; -.
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR003760; Bmp.
DR InterPro; IPR008107; Mycoplasma_p48.
DR InterPro; IPR011050; Pectin_lyas_like.
DR Pfam; PF02608; Bmp; 1.
DR PRINTS; PRO1733; LIPPROTEIN48.
KM Complete proteome; lipoprotein.
SQ SEQUENCE 461 AA; 51096 MW; 6724D4D820809CE4 CRC64;

Query Match 25.6%; Score 552; DB 2; Length 461;
Best Local Similarity 31.2%; Pred. No. 3e-26;
Matches 133; Conservative 82; Mismatches 161; Indels 50; Gaps 11;

QY 13 ADNONKOIT--DVSKISGLVNER-----KSEIMAAKADANKHFGMLMAIVTAGTV 61
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 28 AQNNTKNSNLDSSKITDLSQKEVETQKIVENKIKQASLETK-----VLTITAGSI 82
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 62 NDNSFNQSGWEALIQALATGGEITTS-----VDSSTALEGKYSILANTNK 107
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 83 DDKSFNQGVESQKTLDFDKAVKYSQNKAEHQKLDNYINSAVKOLEQYKVALDRGY 142
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 108 NWVWLSFGQDADTRMLKLPENKQLFTEKNIIILIGIDWTDTE--VIPTRGYINLYTKTE 166
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 143 TTYWLTFTQQNELENEFLINDENNLRREKNEVKLIIGVWAPNANSKIPQGLSILFRTE 202
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 167 EAGLAGYANASFLAKFPSPDPTKRSALVIGGGISPAVTPDIAGYLGIKAMN--LNKSD 224
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 203 EAGGQAGYASADFGLTKYANNEAKRAISAFGGGPAVTPDILNFPESIRAMNSEAERAN 262
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 225 KKTKITTDKLEINLGFVDQSTKRELEQIASKDKPSTLLAVAGPLTEIFSDII---ANQ 281
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 263 KKVYIVSENIIVLTGTF--IPNAEKNEVSVNVETGKSTISLPVAGPFGVVVDVLRKQTS 321
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 282 NDRYLIGVDVDDSLVYTKTKNKKFTSILKNLGYSVFVLSDLTY-----KKSNSRL 333
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
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Db 322 EDRPIVVDVDDQSLSEFNDSKREFTTSIVKNIAFPVQIILALTKDEESYILKGNKFL 381
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 334 AGFEFGKSAIVYIGIKDFVADIADTSLSEGNKKLATEAISEA--KKEFEKTKTIPAE 391
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 382 GS---NPKNLVLRKGLSAKVNITKSKVKSITQDQTSIQKALDKNANPNNSKKIKEM 438
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 392 VRKTL 397
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 439 TNGDLE 444
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 3
ID 06KIQ4 PRELIMINARY; PRT; 491 AA.
ID 06KIQ4
AC 06KIQ4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Unspecified sugar ABC transporter binding protein.
GN OrderedLocustNames=NM080360;
OS Mycoplasma mobile.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=163K / ATCC 43663;
RA Birren B.W., Strange-Thomann N., Smith C., Decaprio D., Fisher S.,
  Butler J., Calvo S., Elkin T., Fitzgerald M.G., Haefer N., Kodira C.D.,
  Major J., Wang S., Wilkinson J., Nicol R., Nussbaum C.;
  Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB017337; AAT7522.1; -.
DR InterPro; IPR008107; Mycoplasma_p48.
DR PRINTS; PRO1733; LIPPROTEIN48.
KM Complete proteome.
SQ SEQUENCE 491 AA; 52817 MW; 2D1C707687771B41 CRC64;

Query Match 21.6%; Score 465.5; DB 2; Length 491;
Best Local Similarity 29.7%; Pred. No. 8.2e-21;
Matches 141; Conservative 80; Mismatches 165; Indels 89; Gaps 18;

QY 15 NOKKOITDVSKISGLVNERSEIMAAKADANKHFGMLMAIVTAGTVNDNSFNQSGWEAL 74
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 32 NTGLRVTDNQVDFDLVASREABPAIQRVANNSLPNSKTLIITLGGVYNDLSFNDSIEAL 91
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 75 QQLGALTG--GEITSVDSSTA---ELEKGYSLANTKNVWVLSGFQGDAPFRWLKIP 129
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 92 LEIGRQTKRGKGNPSFAETTAGTGDQLOQYDQALFFNHKFWVLTFQGDGAFQWQLIGN 151
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 130 NKOLFTEKNIIILIGIDWTDTEENVIPTRGYINLYTKTEBAGWLAGYANASFLAKKFPSPDPT 189
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 152 NRAEFIRKQVILVADWTTLLEVPQGFISIVRTQESSMIVGNVAKFISDHNHN-- 209
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 190 KRAIVIGGSIAPVNDPFIAGYLAGIKAWNLKNS-----DKTKRIT--DKIEI 236
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 210 -RTFNTFGGAPFVNTNFNAGFLQGIIDFN--NSTFLPEBETSIITDKKLSPTGDIINI 266
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 237 NLGFDVQDSTKRELEQIASKDKPST--LLAVAGPLTEIFSDIITANQD--RYLIGVTDQ 293
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 267 NTGPAV-----TPBAATLQSIIVSGTQVFPVAGSLTLLVNSISQNSQGFVIGVDSQ 322
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 294 SLVYTKTKN--FTSILKNLGYSVFVLSDLTY-----TKKSNS 330
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 323 AKAFSPDLATLFFSSVEKNVAGTTVALASLYGTASTDPFNIITGSSSRFIPVTEKNS 382
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 331 RNLAGFEFGKSAIVYIGIR-----FVADIATSLSEGNKKLATEA---ISEAKKEF 380
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 383 SSLP-----LANADITKGFEVSETPVDVGFSSALAGKKTQSLVQANVGRSPAEVAD 437
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 381 -----BEKTK--TIPAEVRKTLAIPEMP--DKQDPKQOESLDKLITDIN 421
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 438 LAASLALFNKNKAKIATIP-----VQIPNPSGGSGSTEQIPNPINELIKKIN 485
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
```

DR InterPro; IPR003760; Bmp.
 DR InterPro; IPR008107; Mycoplasma_p48.
 DR Pfam; PF02608; Bmp; 1.
 DR PRINTS; PR01733; LIPOPROTEIN48.
 DR Lipoprotein; Signal.
 FT SIGNAL 1 22
 SQ SEQUENCE 465 AA; 51149 MW; 60ADS448CFE03C96 CRC64;

Query Match 18.1%; Score 391; DB 2; Length 465;
 Best Local Similarity 31.2%; Pred. No. 3.4e-16;
 Matches 119; Conservative 76; Mismatches 128; Indels 58; Gaps 18;

55 VTAGCTVNDNSFNSGWEALQALGTGGEITVSSTAELEGG-----YSSL 102
 70 ITDGSVHDESFNDSGWEALVAVKVEGLDRAQV-SGNKILRNKYEPKQGLLEATKNA 128
 103 ANTKNVMVLSGFQHGDAFTRLMKIPENK-QLPTEKNIIIGIDMT-----DTENV----- 152
 129 IDSGFRIVLCGFTHQASL---VGLDENYIKIKIDNNIIFTVDPNLETTEDANVKTPEIK 185
 153 -IPGRINLTYTEEGWLAGYANASFLAKKPSDPKRSAYIYGGISPAVDTFAGY 211
 186 KIGGHLVPVIFDTKQALAYLAGALADYFSQVYKQPEKRTIGAFGGIPWPAVSDFTAGT 245
 212 LAGIKANWLKSDKTKITTDKIEINLGFVDVDTSTKERLEQIASKQSPSTLLAVAGPL- 270
 246 FQGIIDNKKHEPKAKTSINETIELNTLF---TSGTQATTAISVYKATSYVAGSL 302
 271 TEIPSDI--IAMONDRYLIGVDTQSLVYTKN-----KPTSLKMLGYSVESVLSDL 323
 303 TDTAKETIKLADK-DKFIIGVDADQ-----KNALKGHRIFTSVMKLIQAVYNNIADL 354
 324 YTKSNSRNL-AGFEFGKAT-VYLGIDK-----RPVDIADTS-LEGNDKLALTEALSEA 376
 355 YSKGENDLDLPGEIGKKNPTVFGYDTEKQYGVATSGLLDDKNDIANKALKDA 414
 377 KKEPEKTKTIPAEVRKTL 397
 415 TAYVQK-KT---EIQKSLK 430

RESULT 7
 052311 PRELIMINARY; PRT; 428 AA.

AC OS2311; (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Membrane lipoprotein P48v.
 OS Mycoplasma fermentans.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 RN NCBI_TaxID=2115;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PG18;
 RA Submitted G. Dyer K. Dujancourt A.;
 RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF036106; AAB99740.1;
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR InterPro; IPR003760; Bmp.
 DR InterPro; IPR008107; Mycoplasma_p48.
 DR Pfam; PF02608; Bmp; 1.
 DR PRINTS; PR01733; LIPOPROTEIN48.
 DR Lipoprotein; Signal.
 SQ SEQUENCE 428 AA; 47862 MW; D9506B817E330EAA CRC64;

Query Match 17.8%; Score 384.5; DB 2; Length 428;
 Best Local Similarity 27.0%; Pred. No. 7.8e-16;
 Matches 116; Conservative 86; Mismatches 157; Indels 71; Gaps 17;
 31 NERKSEIIMAAKADANKH-----FGLNMAIVTAGCTVNDNSFNSGWEAI 74

DB 27 NDNESNISPEKDISKTYTTNANGQVYVNAELLKLPVLTITDEGKIDKSFNQSAFEAL 86
 QY 75 QQLGALTGGEITVSSTAELEGGYSLANTNKVMVLSGFQHGDAFTRLMKIPENKOLF 134
 DB 87 KAIKQGTGILNSVBS-SNPEASYNALSAGHKIWLNVFKHQOSIKQY-IDAHBEEL 143
 QY 135 TEKNIILIGIDMTDENVIPTRGRINLTYTEEGWLAGYANASFLAKKPSDPKRSAYI 194
 DB 144 ERNQIKIIGIDF-DIETREYKM--FYSLOFNKESAPFTGYAISWSEQ---DESKVVA 197
 QY 195 VIGGISPATVDTFAGYLAGIKANLKNSDKTKIT-TDKIEINLGFVDVDTSTKERLEQ 253
 DB 198 SFGGAPPGVTTPEGPAKILLYNQH--KSYKFTTSPVKKIDSGP-----TAGETKMT 250
 QY 254 IAS-----KDRSTLLAVAGPLTEIPSDI IAMONDRYLIGVDTQSLVYTKN 303
 DB 251 VINNVLSSTPADVKNHVLISVAGPAT--FETVKLANKQYVIGVSDGAMT--QDKR 306
 QY 304 FETSILKNLGYSVESVLSDL-----YTKSNSRNLAGEPEFGKSAVYLGIDRF 353
 DB 307 ILTSLVLIHQAVYETLDDILEKEGKPYVVDKADKKWSHFQ-----KEKW 358
 QY 354 VDIADTSLEGNDKL-ATEAISEAKKFEKTKTIPAEVRKTLIEPMD-KOPDQOE 411
 DB 359 IGVAENHFSNTEBQAKINNKIKKAIKMKF-----LPEDFVKYINSRKALDGNKIDNVSE 414
 QY 412 SLQDLITDIN 421
 DB 415 RLEAIIISAIN 424

RESULT 8
 09RGX5 PRELIMINARY; PRT; 428 AA.

AC 09RGX5;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Macrophage activating lipoprotein-404 precursor.
 GN Name=malp; fermentans.
 OS Mycoplasma fermentans.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 RN NCBI_TaxID=2115;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SKS;
 RX MEDLINE=99115554; Pubmed=9916088;
 RA Calcutt M.J., Kim M.F., Kaipras A.B., Muhlradt P.F., Wise K.S.;
 RT "Differential posttranslational processing confers intraspecies
 variation of a major surface lipoprotein and a macrophage-activating
 lipopeptide of Mycoplasma fermentans."
 RT Infect. Immun. 67:760-771(1999).
 RL Infect. Immun. 67:760-771(1999).
 DR EMBL; AF099211; AAD16395.1;
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR InterPro; IPR003760; Bmp.
 DR InterPro; IPR008107; Mycoplasma_p48.
 DR Pfam; PF02608; Bmp; 1.
 DR PRINTS; PR01733; LIPOPROTEIN48.
 DR Lipoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 428 Potential.
 SQ SEQUENCE 428 AA; 47835 MW; D03F0F47EA2B1460 CRC64;

Query Match 17.7%; Score 382.5; DB 2; Length 428;
 Best Local Similarity 27.0%; Pred. No. 1e-15;
 Matches 116; Conservative 87; Mismatches 156; Indels 71; Gaps 17;
 31 NERKSEIIMAAKADANKH-----FGLNMAIVTAGCTVNDNSFNSGWEAI 74
 DB 27 NDNESNISPEKDISKTYTTNANGQVYVNAELLKLPVLTITDEGKIDKSFNQSAFEAL 86
 QY 75 QQLGALTGGEITVSSTAELEGGYSLANTNKVMVLSGFQHGDAFTRLMKIPENKOLF 134

ID	AA127522	PRELIMINARY;	PRT;	491 AA.
AC	AA127522;			
DT	24-MAY-2004	(TREMBLrel. 27, Created)		
DT	24-MAY-2004	(TREMBLrel. 27, Last sequence update)		
DT	24-MAY-2004	(TREMBLrel. 27, Last annotation update)		
DE	Unspecified sugar ABC transporter binding protein.			
CN	MOB0360.			
OS	Mycoplasma mobile 163K.			
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma;			
OC	Mycoplasma mobile.			
OX	NCHI_TaxID=267748;			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=163K;			
RC	STRAIN=163K;			
RA	Bitren B.W., Stange-Thomann N., Smith C., DeCaprio D., Fisher S.,			
RA	Butler J., Calvo S., Elkin T., Fitzgerald M.G., Hafez N., Kodira C.D.,			
RA	Major J., Wang S., Wilkinson J., Nicol R., Nusbaum C.			
RL	Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=163K;			
RA	Jaffe J.D., Church G.M.;			
RL	Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AE017337; AA127522.1; -			
SO	SEQUENCE 491 AA; 52817 MW; 2DC707687771B41 CRC64;			
Query Match	21.6%; Score 465.5; DB 2; Length 491;			
Best Local Similarity	29.7%; Pred. No. 8.2e-21;			
Matches 141; Conservative 80; Mismatches 165; Indels 89; Gaps 18;				
15	NQNKQITPVSKISGLVNRKKEIMAAKADAKHFGELMAIVTAGTVDNDSFGSGWAI 74			
Db	32 NTGLRVTDNOVFRDLVASREAPATQRVANNSLFNSKTLTLITAGGVNDLSFOSINEL 91			
QY	75 QOLGALNG--GETISVDSSTA---ELBKGYSGLANTNGVNVVLSCFOHGDAAFTWLTKE 129			
Db	92 LEIGRQGTGKPGNFSFAETTAGTPDQLQRYDQALFENHKFWLTGFODDGAFQWNLQIGN 151			
QY	130 NKQLFTEKNIIILGIDTDTENVIPITGYINULTYTEBAWGLAGYANASFLAKKFPSDPT 189			
Db	152 NRAERIRQVITIVADMTTNLELVPQGFISINTRYTOSSWIVGNAVAKFISDNHNHN-- 209			
QY	190 KRSAIVIGGGISPAVTDFTIAGLIGIKAMNLIKNS-----DKTKITTT-DKLEI 236			
Db	210 -RTNRTFGGGAPEEYTNAGFLQGLIDFN--NSFLPERGETSTDNKKLSFTPGDIINI 266			
QY	237 NLGPDVODSTSKERLEQASKDKEST--LLAVAGPLTEIFSDIIANQND-RYLIGVDTDQ 293			
Db	267 NTGFAV-----TPPEATAIQSLVSGSTQVFPVAGSLTLLTVNNSIQENSGGVIGVDSDQ 322			
QY	294 SLVYTKTKNKK-FPFSILKNLGYSVPSVLSDLY-----TKSNS 330			
Db	323 AKAPSPDLAKLFSSVEKNVAGATTYAALASLYLGTVSTDPFNITGSSSRPIPVTEKONS 382			
QY	331 RNLAGFERGKSAATVYLIGIDR-----FVDADTSLGENDKKLATEA-----ISPAKKEF 380			
Db	383 SSLP-----LANADITTKGFVSTEVDPVGSKALGKTKIQSLVQAVNGSGFAVAD EY 437			
QY	381 -----EKKTK--TIPAEVAKLTLEIPDM--DKQDPKQDSLDKLTIDN 421			
Db	438 LAASLALFNKKAKKIATIP-----VQIPNFGSGSTPEQIPIPLNELIKIN 485			

ID	Q653B5	PRELIMINARY;	PRT;	468 AA.
AC	Q653B5			
DT	01-OCT-2004 (TREMBLrel. 28, Created)			
DT	01-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE	P48-like protein.			
GN	Name=p48;			
OS	Mycoplasma bovis.			
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.			
OX	NCBI_TaxID=28903;			
RP	SEQUENCE FROM N.A.			
RN	[1]			
RA	Rosati S., Alberti A., Robino P., Pletau M.;			
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY557344; AAT64137.1; -			
SC	SEQUENCE 468 AA; 51175 MW; AA0333F810ED2FFE CRC64;			
	Query Match	19.2%;	Score 414.5;	DB 2; Length 468;
	Best Local Similarity	29.5%;	Pred. No. 1,2e-17;	
	Matches 123; Conservative	77;	Mismatches 140;	Indels 77; Gaps 14
QY	53 AIVTAGTVNDNSFNQSGMEALIQGLATGSEITSV-----DSTAELEGKYS 101			
DB	68 AFITDEGSVHDESFNQSGMEAVHKTISYELGDKAQVSGNKRLRNKVPYEPKKGLASSYKN 127			
QY	102 LANTRKNVWVLSGQHGDAFTRMLKIPENKQLFPEKNIILIGIDMTDENV----- 152			
DB	128 AIDSEFRYIVLCGFTHKAL--YGLPEPYIKIKDNNTVFTIVDFDIQODASTGBPAKA 185			
QY	153 -----IPTGRYINLNYKTEEAGMLAGVNASFLAKKSPEDPTKRSALIVGGISPAVDPFI 208			
DB	186 FVDKIGQGRLLPVLPDTRQAAVYIAGRALADYPSKTYKDNPEKRTIGAFGGIIPWPSVDFI 245			
QY	209 AGYLAGIKAWNLKNSDKKTKITTKIEINLGFVDVDTSTKERLEQASKDPSTLLAVAG 268			
DB	246 AGTQGIILDNKKEHPEAKTKSLNNTIELKTSF---TSEPAVAVAINSVIRKATASYPVAG 302			
QY	269 PLTEIFSDIIANQND--RYLIGVDTDOSLVYTKRN-----KFTSLIKNLGYSVFVLS 321			
DB	303 SLSSDDTAKEIKKLGDKNKFIIGVADQ-----KNALKGRIRFTSVKLLIGQAVYNYVLA 355			
QY	322 DLYNRKKSRL--AGFERGKS-----ATVYLGHKDRVVDIADTS--LEGNDK 366			
DB	356 DLYSGEENSLSLQGFPEIGKNGAKVFGYGENEASKTVGA-----TSGLLDSKND 407			
QY	367 KLAIEAISAEKKPEFEKTKTPAEVEKTL--EIPV-----MPDKDPKQCESLDKLI 417			
DB	408 EIAKKALEAKKYESK-----KAEIQKTLSSGLEBAKKAIGTKMPDPADQFGKMI 459			
RESULT 6				
ID	Q9X775	PRELIMINARY;	PRT;	465 AA.
AC	Q9X775			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	P48 membrane lipoprotein precursor.			
GN	Name=p48;			
OS	Mycoplasma agalactiae.			
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.			
OX	NCBI_TaxID=2110;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20002620; PubMed=10531294;			
RA	Rosati S., Pozzi S., Robino P., Montinaro B., Conti A., Fadda M.,			
RA	Pletau M.;			
RT	"P48 major surface antigen of Mycoplasma agalactiae is homolog to a			
RT	major product of Mycoplasma fermentans and belongs to a selected family			
RT	of bacterial lipoproteins.";			
RL	Infect. Immun. 67:6213-6216(1999).			
DR	EMBL; AJ132423; CAB43718.1; -			
DR	GO; GO:0008289; F:lipid binding; IEA.			

Db 87 KAINKOTGIEINNEPS-SNFESAYNSALSGHKIWLNGFKHQOOSIKOY--IDAAREEL 143
 QY 135 TEKNIITLIGDWTDETVIPTGRYINLTYTEAGWLAGYANASFLAKKPPSDPTKSAI 194
 Db 144 ERNOIKITIGIDF-DIEFEYK--FYSLOPNIKESAFPTTGAIASWSEQ--DESKVVA 197
 QY 195 VIGGISPAYTDFLAGYAGIKAMNLKNSDKTKI--TTDKIEINLGFVDVDTSTKERLEQ 253
 Db 198 SPFGGAFPGVTTTFEGFAKILYVNGH--KSKITYHTSPVKLDSGF-----TAGEKNT 250
 QY 254 IAS-----KDKSTLLAVAGPLTEIFSDIIANONRYLIGVDTDSLYTTTKNK 303
 Db 251 VINNVLSSTPADYKYNPHVILSVAGPAT--FETVRLANKGOYVIGVSDQGM--QDKDR 306
 QY 304 FPTSILKNLGYSVFVSDL-----YTKKSNRNLAGFEFGKKSATVYLGIDRF 353
 Db 307 ILTSVLKHIOAYETLIDLILEKEBGKPYVVKDKADKMSHFQO-----KEKW 358
 QY 354 VDIADTSLGNDKKL-ATEAISEAKKEFEERTKTIPEAEVRYKLEIPEMPD-KOPDKOE 411
 Db 359 IGVAENHFSMTBEQAKINNKIKEMFKE---LPEDFVKYNSDVALKDGKIDNVSE 414
 QY 412 SLDKLITDIN 421
 Db 415 RLRAIISAIN 424

RESULT 9

ID 032417 PRELIMINARY; PRT; 428 AA.
 AC 032417;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE M61Ag.
 OS Mycoplasma fermentans.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 RX NCBI_TaxID=2115;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=98022661; PubMed=9359703;
 RA Matsumoto M., Takeda J., Inoue N., Hara T., Hatanaka M., Takahashi K.,
 RA Nagasawa S., Akedo H., Seya T.;
 RT "A novel protein that participates in nonself discrimination of
 RT malignant cells by homologue complement.";
 RL Nat. Med. 3:1266-1270(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98241611; PubMed=9575196;
 RA Matsumoto M., Nishiguchi M., Kikkawa S., Nishimura H., Nagasawa S.,
 RA Seya T.;
 RT "Structural and functional properties of complement-activating protein
 RT M61Ag, a Mycoplasma fermentans gene product that induces cytokine
 RT production by human monocytes.";
 RL J. Biol. Chem. 273:12407-12414(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Seya T., Matsumoto M.;
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D64083; BAA23530.1; -
 DR EMBL; AB026157; BAA77211.2; -
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR InterPro; IPR003760; Bmp.
 DR Pfam; PF02608; Bmp; 1.
 DR PRINTS; PRO1733; LIPPROTEIN48.
 SQ SEQUENCE 428 AA; 47862 MW; F43B078F21DADDE CRC64;

Query Match 17.6%; Score 379.5; DB 2; Length 428;
 Best Local Similarity 26.7%; Pred. No. 1.6e-15;
 Matches 115; Conservative 88; Mismatches 156; Indels 71; Gaps 17;

QY 31 NEKSEIMAKADANKH-----FGLNMAIVTAGCTVNDNSFNQSGHEAI 74
 Db 27 NNDESINISFKEDISKYTTTNANGQVKNABELLKLPVLTIDEGKIDDSFNQSAFEAL 86
 QY 75 QQLGALTGSEITVSDSTALEGKYSSTANTNKNVWLSGFQHDATTRMLKIPENQOLF 134
 Db 87 KAINKOTGIEINNEPS-SNFESAYNSALSGHKIWLNGFKHQOOSIKOY--IDAAREEL 143
 QY 135 TEKNIITLIGDWTDETVIPTGRYINLTYTEAGWLAGYANASFLAKKPPSDPTKSAI 194
 Db 144 ERNOIKITIGIDF-DIEFEYK--FYSLOPNIKESAFPTTGAIASWSEQ--DESKVVA 197
 QY 195 VIGGISPAYTDFLAGYAGIKAMNLKNSDKTKI--TTDKIEINLGFVDVDTSTKERLEQ 253
 Db 198 SPFGGAFPGVTTTFEGFAKILYVNGH--KSKITYHTSPVKLDSGF-----TAGEKNT 250
 QY 254 IAS-----KDKSTLLAVAGPLTEIFSDIIANONRYLIGVDTDSLYTTTKNK 303
 Db 251 VINNVLSSTPADYKYNPHVILSVAGPAT--FETVRLANKGOYVIGVSDQGM--QDKDR 306
 QY 304 FPTSILKNLGYSVFVSDL-----YTKKSNRNLAGFEFGKKSATVYLGIDRF 353
 Db 307 ILTSVLKHIOAYETLIDLILEKEBGKPYVVKDKADKMSHFQO-----KEKW 358
 QY 354 VDIADTSLGNDKKL-ATEAISEAKKEFEERTKTIPEAEVRYKLEIPEMPD-KOPDKOE 411
 Db 359 IGVAENHFSMTBEQAKINNKIKEMFKE---LPEDFVKYNSDVALKDGKIDNVSE 414
 QY 412 SLDKLITDIN 421
 Db 415 RLRAIISAIN 424

RESULT 10

ID 09RGX4 PRELIMINARY; PRT; 429 AA.
 AC 09RGX4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Macrophage activating lipoprotein-404 precursor.
 GN Name=malD;
 OS Mycoplasma fermentans.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 RX NCBI_TaxID=2115;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MT-2;
 RX MEDLINE=99115554; PubMed=9916088;
 RA Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
 RT "Differential posttranslational processing confers intraspecies
 RT variation of a major surface lipoprotein and a macrophage-activating
 RT lipopeptide of Mycoplasma fermentans.";
 RL Infect. Immun. 67:760-771(1999).
 DR EMBL; AF09212; AAD16396.1; -
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR InterPro; IPR003760; Bmp.
 DR Pfam; PF02608; Bmp; 1.
 DR PRINTS; PRO1733; LIPPROTEIN48.
 KW Lipoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 429 Potential.
 SQ SEQUENCE 429 AA; 47933 MW; B6D08CF975AC3171 CRC64;

Query Match 17.6%; Score 379; DB 2; Length 429;
 Best Local Similarity 26.9%; Pred. No. 1.7e-15;
 Matches 116; Conservative 89; Mismatches 154; Indels 72; Gaps 18;

[illegible]

	Query March	17.6%	Score 379;	DB 2;	Length 429;
	Beet Local Similarity	27.0%;	Pred. No. 1.7e-15;		
	Matches 117; Conservative	88;	Mismatches 151;	Indels	78; Gaps 18;
Oy	31 NERKSEIIMAAADANKH-----FGALNATVYAGTAVDNSNGSGEAI	74			
	: : : :	:	: : : : :		
Dd	27 NNDESNIISPEKEDISKYTTTNANGQVVKNALLKIKLEVLITDEGKIDDKSNGSAFEAL	86			
Oy	75 QQLGLTGTGETSVDSFAALEGGKSSLIANNKKWVWSGCHGAFLRMLKIPENKOLF	134			
Dd	87 KAIKKQTGEILNNVPS-SNEFSAANSLSAGHKITWLNGFGHQOSIQOY--IDAAREEL	143			
	: : : : : : : : : : : : : : : :	:	:	:	:

Qy	135	TEKNIIIIIGDWTDPENVIPTGRYINLVYKTEACGLAGYANASFLAKKEPSPPTGRSAI	194
Db	144	ERNQIKIGIDF-DIETEKYK--FSLQPNIKESAFTTGYALASWSEQ---DESGRYVA	197
Qy	195	VIGGIGISPAVTDPIAGIYLAGIKAMNLKNSDKYTKI-TTDKIEINLGFVDVPTSTKERLEQ	253
Db	198	SFGGAGFPGVLTFFNKGAFKGLIYYNQKH--KSSKIIYHSTPVKRLDSGF-----TAGCKNMY	250
Qy	254	IAS-----KKKSTLLAVAPLPIEIPSDI-IANQNDVYLLGVDPDQSLVYKTKN	302
Db	251	VINNVLSSTPADVKYNPHVILYSVAGPAT--FETVRLANKGGQVIGVDSDDQWT--QDXYD	306
Qy	303	KEFTSIILKNLGYSVSVLSDL-----YTKKSNSENLGAFEGKKSATVYIGIKDR	352
Db	307	RLTSTVLKHRIQAVYETLLDLILEKEGYKPYVVKDKKADKKMSHGQTQ-----KEK	358
Qy	353	FVDIDTSLSEGNDRKL-ATEAISEAKKEF---EKKTKIPIAEVRKTLIEIMPDKQD	407
Db	359	WIGVAENHPSTNEEQAKINNKIKELKMPKELPEDPVKYNISDKVVK-----DGNKID	411
Qy	408	KQGESLDRKLTIDIN 421	
Db	412	NVSERLKALISAIN 425	
RESULT 12			
Q9RGX7	ID	PRELIMINARY;	PRT; 428 AA.
AC	Q9RGX7;		
DT	01-MAY-2000 (TREMblrel. 13, Created)		
DT	01-MAY-2000 (TREMblrel. 13, Last sequence update)		
DT	01-MAR-2004 (TREMblrel. 26, Last annotation update)		
DE	Macrophage activating lipoprotein-404 precursor.		
GN	Name=malp;		
OS	Mycoplasma fermentans.		
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.		
OX	NCBI_TaxID=2115;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=11-29/1;		
RX	MEDLINE=99115534; PubMed=9916088;		
RA	Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;		
RT	"Differential posttranslational processing confers interspecies		
RT	variation of a major surface lipoprotein and a macrophage-activating		
RT	lipopeptide of Mycoplasma fermentans."		
RL	Infect Immun. 67:760-771(1999).		
DR	EMBL, AF099209; AAD16393.1;--		
DR	GO; GO:0008289; F:lipid binding; IEA.		
DR	InterPro; IPR003760; Bmp.		
DR	InterPro; IPR008107; Mycoplasma_p48.		
DR	Pfam; PF02608; Bmp; 1.		
DR	PRINTS; PR01733; LIPOPROTEIN48.		
DR	lipoprotein; Signal.		
FT	SIGNAL		
FT	CHAIN		
FT	1 25 24		
FT	potential.		
FT	macrophage activating lipoprotein-404.		
SEQUENCE	428 AA; 47960 MW; D6569C0BA69CFE1 CR664;		

[illegible]

[illegible]

RESULT 13	
ID	Q9RGX3
AC	Q9RGX3
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	Macrophage activating lipoprotein-404 precursor.
GN	Name=malp:
OS	Mycoplasma fermentans.
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX	NCBI_TaxID=2115;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=K7;
RX	MEDLINE=99115554; PubMed=9916088;
RA	Calcutt M.J., Kim M.P., Karpas A.B., Muhradt P.F., Wise K.S.;
RT	"Differential posttranslational processing confers intraspecies
RT	variation of a major surface lipoprotein and a macrophage-activating
RT	lipopeptide of Mycoplasma fermentans. "
RL	Infect. Immun. 67:760-771(1999).
DR	EMBL: AF099213; AAD16397.1: -;
DR	GO: GO:0008289; F:lipid binding; IEA.
DR	InterPro: IPR003760; Bmp.
DR	InterPro: IPR008107; Mycoplasma_p48.
DR	Pfam: PF02608; Bmp; 1.
DR	PRINTS; PR01733; LIPPROTEIN48.
KW	Lipoprotein; signal.
FT	SIGNAL
FT	CHAIN 1 24
FT	POTENTIAL
QO	SEQUENCE 428 AA; 47875 MW; C7A536B409A60132 CRC64;
	macrophage activating lipoprotein-404.

[illegible]

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QY 304 FETSLIKULGVSEFVLSDL-----YTKKSNSRLAGPEFQKSAATVYLGIDHP 353
Db 307 ILTSLYKHI KOAVVETTLDDLIIKEEGEYPIVVKDKKADKKMSHFSTQ-----KEKX 358
QY 354 VDIADTSLGNDKUL-ATEAISAKKEFEFEKTKTIPAEVVRKTLGIPEMPD-KQDPKQOE 411
Db 359 IGVAENHSNTEQAKINKKIKEAIKMFKE---LPEDFVKTINSKALKDKGKINDVSE 414
QY 412 SLDDKLITDIN 421
Db 415 RUEAITSAIN 424

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RESULT	14
Q9R3N6	
ID	Q9R3N6
AC	Q9R3N6;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE	Lipoprotein MALP-40a precursor (Macrophage activating lipoprotein-40a precursor).
GN	Name=malp; Synonyms=malp;
OS	Mycoplasma fermentans.
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX	NCBI_taxid=2115;

RP SEQUENCE FROM N.A.
RC STRAIN=PG18, M39A, and M70B;
RX MEDLINE=99115554; PubMed=9916088;
RA Calcutt M.J., Kim M.F., Karnas A.B., Muhlradt P.F., Wise K.S.;
RT "Differential posttranslational processing confers intracellular
RT variation of a major surface lipoprotein and a macrophage-activating
RT lipopeptide of *Mycobacterium lemurum*.";
RL Infect. Immun. 67:760-771(1999).
DR EMBL; AF100324; AAD25736.1; -;
DR EMBL; AF099214; AAD16398.1; -;
DR EMBL; AF099215; AAD16399.1; -;
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPRO03760; Bmp.
DR InterPro; IPRO08107; Mycoplasma_p48.
DR Pfam; PF02608; Bmp; 1.
DR PRINTS; PRO1733; LIPROTEIN8.
KM Lipoprotein; Signal. 24
FT SIGNAL 1
FT CHAIN 25
SQ SEQUENCE 428 AA; 47863 MW; 59808324E218F03C CRC64;

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Query Match      17.3% Score 373.5; DB 2; Length 428;
Best Local Similarity 26.7%; Pred. No. 3.8e-15;
Matches 115; Conservative 87; Mismatches 157; Indels 71; Gaps 177;

QY 31 NERKSEIMAAKADANKH-----PGLNMAIVTAGATVNDNSFNQSGWEAI 74
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 27 NNDSNSISFKEKDISKTYTTNANKQVYKNNELLKLPVLTIDBGKIDDKSFFNQSAPFAL 86
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 75 QOLGALTGEITSVDSSTAIEGKYSSLIANTNNKVVWLSGFGHDATRWLIKIDENKOLF 134
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 87 KAINKQTGIEINSVPS-SNFSASVNSALSGHKIMWLNKFGHOOSIKQY--IDAHEEL 143
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 135 TEKNIILIGIMWTENTENVIPTRIRINLTKYTEEGMVLAGYNAABFLAKFFSDPTKRAI 194
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 144 ERNOQKIIGIDP-DIETERYKN--FVSLQFNKEKSAFTTGYVIAWLSLQ---DESKRYVA 197
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 195 VIGGIGSPAVDPFLAGYLAGIKANNLNKSDKTKI--TTDKIEINLGFVQDQTSKERLEQ 253
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 198 SFGVGAFFGVTTNEGFAKGLIYNNOKH--KSKKIYHTSPKULDSGF-----TAGKKRNT 250
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 254 IAS-----XDKESTLLAVAGPLTEIFSDIIANQNDRYLLIGVDTDQSLVYTKTKNK 303
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 251 VINNVLSTPADVKNYPHVLISVAGPAT--FETVRLANKQGYVIGVSDQGMV--QDKDR 306
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 304 FFTSLIKNLGYSVESVLSDL-----YTKSNSBNLNAEGFEFKKSATVYLGIDKRF 353
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 307 ILTSVLKHIQAVYETLIDLLEKEGKPYVVDKAKKWSHFQ-----KRW 358
QY 354 VDIADTSLLEGNDKLT-ATEAISBAKEPEEKTITIPABEVKTLIPEMPD-KOPDKQE 411
Db 359 IGVNENHPSNTEEQAKINNKIKKAIKMFKE---LPEDPVKYNISDKALKDKNKIDNVSE 414
QY 412 SLDKLITDIN 421
Db 415 RLEAIIISAIN 424

RESULT 15

Q8RCH2 PRELIMINARY; PRT; 352 AA.
ID Q8RCH2
AC Q8RCH2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Surface lipoprotein.
GN Name=Med; OrderedLocustNames=TT00457;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL: AE013017; AM23740.1; -
DR GO: GO:0008289; F:lipid binding; IEA.
DR InterPro: IPR003760; Bmp.
DR Pfam: PF02608; Bmp; 1.
KW Complete proteome; Lipoprotein.
SQ SEQUENCE 352 AA; 38052 MW; DCA7990EA271A23B CRC64;

Query Match 10.6%; Score 229.5; DB 2; Length 352;

Best Local Similarity 26.0%; Pred. No. 2.9e-06;
Matches 94; Conservative 55; Mismatches 158; Indels 55; Gaps 13;

QY 26 ISGLVNERKSEIMAK--ADANKHFGINMAIVTAGTVNDNPFNOSGWEAIOQLGALTGG 83
Db 22 LSGGSSKTKQESTPQOTTEANKKPKFVGLVTDVGGINDRSPNOMAYEGIQRAKEIGV 81
QY 84 EITSVDS-STALEGKYSSLANTNKANVVLGFOHGDAPTRMLKIPENKQLFTEKNITL 142
Db 82 TVNVIOGKQMTDVPNLTNFAQGYDLVISGFMMHDA-----TEEVSQKFPNTKFLII 135
QY 143 GIDWTDENVIPTGRYINLTYTEAGWLAGYANASFLAKKPSDPTKSAIV--IGGI 200
Db 136 DSEITDPPNV-----ASMPKEQEVGLAG--ALAGLVEKEKVKVGTNIIIGAVGQM 187
QY 201 SPATYDPIAGLAGIKAMNLTNKSDDKTKITTDKIEINLGFVDPVOSTKERLEQIASKDXP 260
Db 188 IPPVDRFIAGIQGAKAVN-----PIKILINVTNNPNDPAAGKALTOISOGA 237
QY 261 STLLAVAGPLTEIFSDII--ANQNDRYLIGVTDQSLVYTKNKKFPTSILKNLGYSVFS 318
Db 238 EIIPOVAGGTGE--GVYKAQOEKNLYAIGVDADQSYL--APDNVLTSAVKRVDAVYD 291
QY 319 VLSD-----LYTKKSNSRLAGFEFEKKSATYVLGIDKRF---VDIADTSLBGN 364
Db 292 VIKDALNGNEKSGIMYFDLKN---GVGLGKINKNDVPQSIIDQVNOIAKDIIDGKIQVS 347
QY 365 DK 366
Db 348 DK 349

Search completed: December 18, 2004, 01:26:33
Job time : 121.543 secs